

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:57:41 ; Search time 37.6351 Seconds
(without alignments)
3819.179 Million cell updates/sec

Title: US-09-647-978A-2

Perfect score: 2832

Sequence: 1 MSDGTASARSSPLDRPAF.....LSCAEESDPCRELTPDKS 557

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|---------------------|
| 1 | 2832 | 100.0 | 557 | 11 | Q9WV89 | Q9WV89 mus musculus |
| 2 | 2522 | 89.1 | 533 | 11 | Q8CFL1 | Q8CFL1 mus musculus |
| 3 | 755 | 26.7 | 245 | 4 | Q8LVZ5 | Q8LVZ5 homo sapien |
| 4 | 195.5 | 6.9 | 1492 | 4 | Q9NU93 | Q9NU93 homo sapien |
| 5 | 192.5 | 6.8 | 2484 | 6 | Q28C06 | Q28C06 bos taurus |
| 6 | 187.5 | 6.6 | 1427 | 4 | Q9NU94 | Q9NU94 homo sapien |
| 7 | 183.5 | 6.5 | 1333 | 4 | Q9NU91 | Q9NU91 homo sapien |
| 8 | 183 | 6.5 | 1829 | 11 | Q35889 | Q35889 rattus norv |
| 9 | 182.5 | 6.4 | 883 | 4 | Q96MN6 | Q96MN6 homo sapien |
| 10 | 181.5 | 6.4 | 1410 | 4 | Q9NSN7 | Q9NSN7 homo sapien |
| 11 | 178 | 6.3 | 1296 | 4 | Q9NU90 | Q9NU90 homo sapien |
| 12 | 177.5 | 6.3 | 1663 | 11 | Q35890 | Q35890 rattus norv |
| 13 | 175 | 6.2 | 1624 | 5 | Q9U679 | Q9U679 strongyloce |
| 14 | 174 | 6.1 | 1136 | 4 | Q8TEW8 | Q8TEW8 homo sapien |
| 15 | 171.5 | 6.1 | 1205 | 4 | Q96NX7 | Q96NX7 homo sapien |
| 16 | 171.5 | 6.1 | 1205 | 4 | Q81UC7 | Q81UC7 homo sapien |

| | | | | | | |
|----|-------|-----|------|----|--------|---------------------|
| 17 | 168 | 5.9 | 1104 | 4 | Q81UC9 | Q81UC9 homo sapien |
| 18 | 167 | 5.9 | 1116 | 3 | Q9HGL2 | Q9HGL2 schizosacch |
| 19 | 165 | 5.8 | 933 | 5 | Q9W3V2 | Q9W3V2 drosophila |
| 20 | 165 | 5.8 | 2176 | 5 | O46112 | O46112 drosophila |
| 21 | 165 | 5.8 | 2460 | 11 | O64512 | O64512 mus musculus |
| 22 | 164.5 | 5.8 | 561 | 5 | Q95Q64 | Q95Q64 caenorhabdi |
| 23 | 164.5 | 5.8 | 658 | 5 | Q95Q66 | Q95Q66 caenorhabdi |
| 24 | 164.5 | 5.8 | 721 | 5 | P91146 | P91146 caenorhabdi |
| 25 | 164 | 5.8 | 927 | 11 | O62402 | O62402 mus musculus |
| 26 | 163.5 | 5.8 | 611 | 5 | Q9V6P9 | Q9V6P9 drosophila |
| 27 | 163.5 | 5.8 | 1459 | 3 | P87198 | P87198 ustilago ma |
| 28 | 163 | 5.8 | 411 | 4 | Q8NEN7 | Q8NEN7 homo sapien |
| 29 | 163 | 5.8 | 624 | 4 | Q96DK9 | Q96DK9 homo sapien |
| 30 | 162.5 | 5.7 | 963 | 4 | Q96HN5 | Q96HN5 homo sapien |
| 31 | 161.5 | 5.7 | 1220 | 13 | Q8JFT5 | Q8JFT5 brachydanio |
| 32 | 161.5 | 5.7 | 1721 | 13 | Q8JFT4 | Q8JFT4 brachydanio |
| 33 | 160.5 | 5.7 | 1006 | 4 | Q96157 | Q96157 homo sapien |
| 34 | 160.5 | 5.7 | 1871 | 5 | Q8IR54 | Q8IR54 drosophila |
| 35 | 160.5 | 5.7 | 1889 | 4 | Q9H430 | Q9H430 homo sapien |
| 36 | 160.5 | 5.7 | 2010 | 4 | Q9P216 | Q9P216 homo sapien |
| 37 | 160.5 | 5.7 | 2328 | 5 | Q9VY43 | Q9VY43 drosophila |
| 38 | 160.5 | 5.7 | 2360 | 5 | Q8IR55 | Q8IR55 drosophila |
| 39 | 160 | 5.6 | 888 | 5 | Q8IP21 | Q8IP21 drosophila |
| 40 | 160 | 5.6 | 930 | 5 | Q8IP22 | Q8IP22 drosophila |
| 41 | 160 | 5.6 | 1103 | 5 | Q8MR15 | Q8MR15 drosophila |
| 42 | 160 | 5.6 | 1658 | 5 | Q9BIC1 | Q9BIC1 caenorhabdi |
| 43 | 160 | 5.6 | 1666 | 5 | Q9XY66 | Q9XY66 caenorhabdi |
| 44 | 160 | 5.6 | 2162 | 5 | Q9VQM0 | Q9VQM0 drosophila |
| 45 | 159.5 | 5.6 | 574 | 11 | Q8RID2 | Q8RID2 mus musculus |

ALIGNMENTS

RESULT 1

Q9WV89 PRELIMINARY; PRT; 557 AA.
AC Q9WV89
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Syntaxin4-interacting protein synip.
GN STXBP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99322657; PubMed=10394363;
RA Min J., Okada S., Kanzaki M., Elmendorf J.S., Coker K.J., Ceresa B.P.,
RA Syu L.J., Noda Y., Saltiel A.R., Pessin J.B.;
RT "Synip: a novel insulin-regulated syntaxin 4-binding protein mediating
RT GLUT4 translocation in adipocytes.";
RL Mol. Cell 3:751-760(1999).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF152924; AAD43533.1; --
DR MGD; MGI:1342296; Stxbp4.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00397; WW; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00456; WW; 1.
DR PROSITE; PSS0106; PDZ; 1.
DR PROSITE; PSS0159; WW DOMAIN 1; 1.
DR PROSITE; PSS0020; WW DOMAIN 2; 1.
SQ SEQUENCE 557 AA; 61688 MW; 9211A8B02AF8EC96 CRC64;

Query Match 100.0%; Score 2832; DB 11; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.1e-157;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | |
|----------|-----|--|-----------------------------------|-------------|---------|
| Qy | 1 | MSDGTASARSSPLDRDPAFRVI | VTTKETGLGLKILGGINRNSGPLYI | HEVTPGSDCYK | 60 |
| Db | 1 | MSDGTASARSSPLDRDPAFRVI | VTTKETGLGLKILGGINRNEGPLYI | HEVTPGSDCYK | 60 |
| Qy | 61 | DGRLKPGDOLVINKESMIGVSFEAKSII | TRAKLRSESPWEIAFIRKSYCGHPGNIC | 120 | |
| Db | 61 | DGRLKPGDOLVINKESMIGVSFEAKSII | TRAKLRSESPWEIAFIRKSYCGHPGNIC | 120 | |
| Qy | 121 | PSPOVSEDCGPOTSTFTLLSPSETLL | PKTSSTTQTQDSTFPCKAIQTKPEHDKTEHP | 180 | |
| Db | 121 | PSPOVSEDCGPOTSTFTLLSPSETLL | PKTSSTTQTQDSTFPCKAIQTKPEHDKTEHP | 180 | |
| Qy | 181 | ITSLDNSPADTNSADIAPAWTDDSG | POCKISLNPVRLKAEKLEMANLYLGIOPTKEOR | 240 | |
| Db | 181 | ITSLDNSPADTNSADIAPAWTDDSG | POCKISLNPVRLKAEKLEMANLYLGIOPTKEOR | 240 | |
| Qy | 241 | EALREOVQADSKGTGTFQVARSFLC | LODEVNVGVGHEIPIISLDQSLPCDSEADE | 300 | |
| Db | 241 | EALREOVQADSKGTGTFQVARSFLC | LODEVNVGVGHEIPIISLDQSLPCDSEADE | 300 | |
| Qy | 301 | VGKLROERNAALAEERNVLKEKLLSE | KHRKQLIEELQNVKQEKAKAAVAETRALRSIH | 360 | |
| Db | 301 | VGKLROERNAALAEERNVLKEKLLSE | KHRKQLIEELQNVKQEKAKAAVAETRALRSIH | 360 | |
| Qy | 361 | EAAQROAHQEMDYBEVIRLLEAEVSE | LKALADYSQNKESVQDLRKRVTVLDCOLRS | 420 | |
| Db | 361 | EAAQROAHQEMDYBEVIRLLEAEVSE | LKALADYSQNKESVQDLRKRVTVLDCOLRS | 420 | |
| Qy | 421 | EWAKAFKASTERLGLGFTAEATQEV | LLDSSAPLSTLSERRAVLASQTSPLPARNGRSP | 480 | |
| Db | 421 | EWAKAFKASTERLGLGFTAEATQEV | LLDSSAPLSTLSERRAVLASQTSPLPARNGRSP | 480 | |
| Qy | 481 | TLLSEKELVSRVRAILDMDCPLCYGE | BAAYTADGIKYFINHVTTQTSWIHPVMSALN | 540 | |
| Db | 481 | TLLSEKELVSRVRAILDMDCPLCYGE | BAAYTADGIKYFINHVTTQTSWIHPVMSALN | 540 | |
| Qy | 541 | AESEEDCPRELTPDKS | 557 | | |
| Db | 541 | AESEEDCPRELTPDKS | 557 | | |
| RESULT 2 | | | | | |
| Q8CFL1 | | | | | |
| ID | | PRELIMINARY; | | PRT; | 533 AA. |
| AC | | Q8CFL1; | | | |
| DT | | 01-MAR-2003 (TEMBLrel. 23, Created) | | | |
| DT | | 01-MAR-2003 (TEMBLrel. 23, Last sequence update) | | | |
| DT | | 01-MAR-2003 (TEMBLrel. 23, Last annotation update) | | | |
| DE | | Similar to syntaxin binding protein 4. | | | |
| OS | | Mus musculus (Mouse) | | | |
| OC | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| NCBI | | TaxID=10090; | | | |
| RN | | (1) | | | |
| RP | | SEQUENCE FROM N.A. | | | |
| RC | | STRAIN=C57BL/6J; TISSUE=Thymus; | | | |
| RA | | Strausberg R.; | | | |
| RL | | Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases. | | | |
| DR | | EMBL; BC032881; AAH32881.1; -. | | | |
| SQ | | SEQUENCE 533 AA; 58591 MW; 8B6BC19511E3AF09 CRC64; | | | |

| | | | |
|--|---|---|-----|
| Qy | 121 | PSQVSEDCGPGTSTTTLLSSPSETLLPKTSTPTQDSTTFPSCKAIQTKPEHDKTEHSP | 180 |
| Db | 121 | PSQVSEDCGPGTSTTTLLSSPSETLLPKTSTPTQDSTTFPSCKAIQTKPEHDKTEHSP | 180 |
| Qy | 181 | ITSLDNSPADTSNADTAPAWTDDSGPQGI SLNPSVRLKAEKLEALNVLGIQPTKEOR | 240 |
| Db | 181 | ITSLDNSPADTSNADTAPAWTDDSGPQGI SLNPSVRLKAEKLEALNVLGIQPTKEOR | 240 |
| Qy | 241 | EALREQVQADSKGTGFGFVQVARSFLCQLQDEVNVGVHEIPSIIDSQLPCDSLEADE | 300 |
| Db | 241 | EALREQVQADSKGTGFGFVQVARSFLCQLQDEVNVGVHEIPSIIDSQLPCDSLEADE | 300 |
| Qy | 301 | VGKLRQERNAALEERNVLKEKLESKHKRKOLTEEQNVKQEKAKAAVESTRALRSIHILA | 360 |
| Db | 301 | VGKLRQERNAALEERNVLKEKLESKHKRKOLTEEQNVKQEKAKAAVESTRALRSIHILA | 360 |
| Qy | 361 | EAARQAHGEMDYEYVIRHLEAEVSELKAQLADYSDONKESVQDLRKRVTVILDCOLRKS | 420 |
| Db | 361 | EAARQAHGEMDYEYVIRHLEAEVSELKAQLADYSDONKESVQDLRKRVTVILDCOLRKS | 420 |
| Qy | 421 | EMARKAFKASTERLLGFI EAIQEVILDS SAPISTLSERRAVILASQTS LPLAANGRSFPA | 480 |
| Db | 421 | EMARKAFKASTERLLGFI EAIQEVILDS SAPISTLSERRAVILASQTS LPLAANGRSFPA | 480 |
| Qy | 481 | TLLESKELVRSVRILDMDC 501 | |
| Db | 481 | TLLESKELVRSVRILDMDC 501 | |
| RESULT 3 | | | |
| Q81VZ5 | | | |
| Id | Q81VZ5 | PRELIMINARY; PRT; 245 AA. | |
| AC | Q81VZ5 | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Created) | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | |
| DE | Similar to syntaxin binding protein 4. | | |
| OS | Homo sapiens (Human) | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| OX | NCBI_TaxId=9606; | | |
| RN | [1] | | |
| RC | SEQUENCE FROM N.A. | | |
| RC | TISSUE=Eye; | | |
| RA | Strausberg R; | | |
| RL | Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; BC041465; AAH41465.1; - | | |
| SQ | SEQUENCE 245 AA; 26974 MW; 4E92DD8BFD27DF79 CRC64; | | |
| Query Match | | | |
| Best Local Similarity 67.3%; Score 755; DB 4; Length 245; | | | |
| Matches 165; Conservative 23; Mismatches 49; Indels 8; Gaps 5; | | | |
| Qy | 78 | MIGVSEERAKSIITRAKL--RSESPHEIAFIROKSYCGHPGNICCPG--POVSEDCGPGTS | 134 |
| Db | 1 | MIGVSEERAKSIITRAKLSTRLESAGEIAFIROKSDNIQIENLSCISLIEASGEYGPAS | 60 |
| Qy | 135 | TFTLLSSPSETLLPKTSTPTQDSTTFPSCKAIQTKPEHDKTEHSPITSLDNGSPADTNSA | 194 |
| Db | 61 | TLSLFSSPPPEILIPKTSSTPTKNTNDILSSC--EIKTGYNKTVQIPITS-ENSTVGLSNT | 116 |
| Qy | 195 | DIAPAWTDDSGPQGI SLNPSVRLKAEKLEALNVLGIQPTKEQREALREQVQADSKGT | 254 |
| Db | 117 | DVASAT-ENYIGQEIKISLNPSVRFKAEKLEALNVLGIQPTKEQHQALRQQVQADSKGT | 175 |
| Qy | 255 | VSRGDFVQVARSFLCQLQDEVNVGVHEIPSIIDSQLPCDSLEADEVGKLRQERNAALEE | 314 |
| Db | 176 | VSRGDFVQVARNLFCQLQDEVNVGAHEISNILDSQLPCDSSEADEMERLKCERDDALKE | 235 |
| Qy | 315 | RNVLK 319 | |
| Db | 236 | VNTLK 240 | |


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QY 126 SEDCG-----PQSTSTPILLSSPSETILLPKTSSPTQDSD----- 159
Db 780 SDRGSGKPRPKSEGFELYNSTONGSPSPQLPWAIESEPKPLPGDRLMKRNRADHRSS 839
QY 160 -----TF 161
Db 840 PNVAQNPPSPGKSAYASGTTAKITSVSTGNLCTEETPPRPEAVPIPTQTYTREYTF 899
QY 162 PSCKA-----IQTKPE-HDKTEHSPI----- 181
Db 900 PASKSQDRMAPPONMYPNIEKPHMTDSNHSSIAIQRVTRSQEELREDKAYQLERHRIE 959
QY 182 -----TSLDSPA-----DTSNADIAPAWTDDSDGPOCK----- 210
Db 960 AAMDRKSDSDMWINQSSSLDSSSQEHLNHSKSVTPASTLTGSGP-GRWKTAAIPAT 1018
QY 211 -ISLNPVR-----LKAEKLEMAL-----NYLGIQPT----- 236
Db 1019 PVAVSQPIRTDLPPLPPPPVHVAGDFGMSMDLPLPPPPSANQIGLPSAQVAAAERRKR 1078
QY 237 -----KEQREALRE-----QVQADSKGTVSGDFV----- 261
Db 1079 BEHQWYEKAKLEERERKRQERKLCQMTQSLNPAPSPPLTAQOMKEKPESTLQR 1138
QY 262 -----QVARSFLCLQDEVNNGVHIEPISILDSQLLPCDSLEADEVGKLRQERN 309
Db 1139 PQETVIRELQPOQOPRTIERRDQYITVSKELSS---GTVCPPDPKWRDAKEKLEKQOQ 1195
QY 310 AALEERNVLEKLESKHKQLIEBLONVQKAEKAVAEETRALRSRI-----HLAEA 362
Db 1196 MHIVD-----MLSKETIQELQSKPDRSAESDRLRKLMLEWQFKRLQOES 1239
QY 363 AQROAHQEMDYEE-----VIRLLEAEVSELKAO-----LADYSDQNKESVQD 405
Db 1240 KOKD-----EDDEEEDDDVTMLIMQRLAEARRARTAMPAPSVLDLLQDEERRQOQLEE 1295
QY 406 LRKRVTVLDCOLKSEKSEKAFKASTER 433
Db 1296 MKKREA--EDRARQEEERQEEERTKR 1321

RESULT 11
Q9NU90
ID Q9NU90 PRELIMINARY; PRT; 1296 AA.
AC Q9NU90;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE DJ470824.1.1 (Myeloid/lymphoid or mixed-lineage leukemia (Trithorax
DE (Drosophila) homolog), translocated to, 4 (AF-6) (Isoform 1))
DE (Fragment).
GN MLLT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AL049698; CAB76852.1; -.
DR HSSP; Q12923; 3PDZ.
DR InterPro; IPR002710; DIL.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF01843; DIL; 1.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS50106; PDZ; 1.
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FT NON TER 1 1
SQ SEQUENCE 1296 AA; 145808 MW; 9PECCF3CA67D19EC CRC64;
Query Match 6.3%; Score 178; DB 4; Length 1296;
Best Local Similarity 18.5%; Pred. No. 0.043;
Matches 110; Conservative 94; Mismatches 194; Indels 198; Gaps 21;
QY 11 SSPLDRDPAPRVITVTKETGLGKILGGINRNEGPL-VYIHEVIGGDCYKGRKLPQGO 69
Db 666 AQPLREPIIITVLKQMGSLVAAGACQDKLGIYKSVVGGADVDGRLAAGDQ 725
QY 70 LVSINKESIGVSFEBAKSIITRAKLRSPEWIAPIRQKS-YCGHPGNICPSP---QV 125
Db 726 LLSVDRGSLVGLSQEAAELMTKTS-SVVTLEVA-XQGIYHGLATLLNQSPMWQRI 781
QY 126 SEDCG-----PQSTSTPILLSSPSETILLPKTSSPTQ----- 155
Db 782 SDRGSGKPRPKSEGFELYNSTONGSPSPQLPWAIESEPKPLPGDRLMKRNRADHRSS 841
QY 156 -----TQDSTFPSCAKAIQTKPEHDKTEHSPTISLDNS----- 187
Db 842 PNVAQNPPSPGKSAYASGTTAKITSVSTGNLCTEETPPRPEAVPIPTQTYTREYTF 901
QY 188 PADTSNADIAP---AWTDDSGP-----OGKISLNPVSRLKAEKLE 225
Db 902 PASKSQDRMAPPONMYPNIEKPHMTDSNHSSIAIQRVTRSQEELREDKAYQLERHRIE 961
QY 226 MALN-----YLGIOPTKEQREALREQVQADSKGTVS----- 256
Db 962 AAMDRKSDSDMWINQSSSLDSSSQEHLNHSKSVTPASTLTGSGPGRWKTAAIPATP 1021
QY 257 -----FGDFVQVARSFLCLQDEVN-VGVHIEPISILDSQLLPC 293
Db 1022 VAVSQPIRTDLPPLPPPPVHVAGDFGMSMDLPLPPPPSANQIG---LPS---AQVAAA 1075
QY 294 DSLEAEVGLKRLERNAALEERNVLK-----EKL 322
Db 1076 ERKRBEHQWYEKAKLEERERKRQERKLCQMTQSLNPAPSPPLTAQOMKEKPEP 1335
QY 323 LESEKHKQLIEBLONVQKAEKAVAEETRALR-----SRHLAEAAQROAHQEMDYEE-- 376
Db 1136 STLQRPQETVIRELQ-POQOPRTI--ERRDLQVITVSKELSSGDSLSLDPKWRDAKEKL 1192
QY 377 -----VIRLLEAEVSELKAOQLADYSDQNKESVQDLRKRVTVLDCOLKSEMARK 425
Db 1193 EKQOMQHIVDMLSKETIQELQSK-----PDRSASESDRLRKLMLLEWQFKRLQOESKQ 1244

RESULT 12
Q35890
ID Q35890 PRELIMINARY; PRT; 1663 AA.
AC Q35890;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE S-Afadin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97477397; PubMed=9334353;
RA Mandai K., Nakanishi H., Satoh A., Obaishi H., Wada M., Nishioaka H.,
RA Itoh M., Mizoguchi A., Aoki T., Fujimoto T., Matsuda Y., Tsukita S.,
RA Takai Y.;
RT "Afadin: A novel actin filament-binding protein with one PDZ domain
RT localized at cadherin-based cell-to-cell adherens junction.";
RL J. Cell Biol. 139:517-528(1997).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; U83231; AAC53391.1; -.
DR HSSP; Q12923; 3PDZ.
DR InterPro; IPR002710; DIL.
```


| | |
|--|---|
| GN | PAR3L |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; |
| OC | Zurkayota; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| NB | NCBI TaxID=9606; |
| OX | [1]_TaxID=9606; |
| RN | SEQUENCE FROM N.A. |
| RP | Gao L., Macara I.G., Joberty G.; |
| RT | "Multiple splice variants of PAR3 and of a novel related gene, PAR3L, |
| RT | produce functionally different proteins."; |
| RL | Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases. |
| CC | -!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS. |
| EMBL: | AF466152: AAL79827.1; .. |
| DR | InterPro: IPR001478; PDZ. |
| DR | Pfam: PF00595; PDZ; 3. |
| DR | SMART: SM00228; PDZ; 3. |
| DR | PROSITE: PS50106; PDZ; 3. |
| SQ | SEQUENCE 1136 AA; 124884 MW; DE734844F61CBB6B CRC64; |
| | |
| Query Match 6.1%; Score 174; DB 4; Length 1136; | |
| Best Local Similarity 19.9%; Pred. No. 0.063; | |
| Matches 85; Conservative 59; Mismatches 130; Indels 154; Gaps 16 | |
| | |
| QY | 30 GLGKILGGINRNEGP--LVYIHEVIFGGCYKDGRLKPGDQLVSINKESMIGVSFEAK 87 |
| Db | GLGVSLKGNGKSRETGTDLGIFIKSIHGGAFAFGDRLRMNDQLIAVNGESLLGKSNHEAM 567 |
| | |
| QY | 88 SIITRAK-----LRSESPWEIAFIROKSYCG----- 113 |
| Db | ETLRSSMSMEGNIRMIOLVILRRPFRPE-----DPAECGAFSKPCFENCQNAVTTSR 622 |
| | |
| QY | 114 -----HPGNICCPSPQS-----EDCGPTSTFTILL 139 |
| Db | NDNSILHLPLGTCSPODKQGKLLPDCGMAESEVPSPTPHSALGLGLEDYSHSSGVDSAV 682 |
| | |
| QY | 140 SPSSTLLPKTSSTP--QTOSTTFSPCKAIOKPEHKTEHSPIITSLDNSPADTSNADIA 197 |
| Db | VYPDQHINFR-SVTPAROPESINLKASMDLVDPDESKV-HSLAGOKSGLSDKMSHQSG 740 |
| | |
| QY | 198 PAWTDDSDGPOCKISLPNVSLKAELMALNYLGIOPTKEQ-----REALREQ 246 |
| Db | GA-INCESAPQGNSELE-DMENKARK-----VKTKTEKKKKVEKGLKVKEKKKE 789 |
| | |
| QY | 247 VOADSKGTVSFGDFVOVARSAFLCLQDEVNVGVHEIPSLDLSQLLPDSEADVGKLKQ 306 |
| Db | ENEDPERKIKKKGFAMLR-----FOKKKE 814 |
| | |
| QY | 307 ERNAALEERNVLKELLSEKHKXKLTIELONVKORAKAVAETRALRSRIHLAEAAQCRC 366 |
| Db | DGKGABOKGTLKHGGLRE-----ELEKKMKERERIGAKHQEUR-----EQO 857 |
| | |
| QY | 367 AHGMENDY 374 |
| Db | ARGL-LDY 864 |

RESULT 15
Q96NX7
ID Q96NX7 PRELIMINARY; PRT; 1205 AA.
AC Q96NX7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Partitioning-defective 3-like protein splice variant a.
OS PAR3L.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT Gao L., Macara I.G., Joberty G.;
RA "Multiple splice variants of Par3 and of a novel related gene, Par3L,

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RT produce functionally different proteins." ;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDAJ databases.
CC -!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
DR EMBL; AF428250; AAL30664.1 ; -.
DR Genew; HGNC:14446; ALS2CR19.
DR InterPro: IPR001478; PDZ.
DR Pfam; PF00595; PDZ; 3.
DR SMART; SM00228; PDZ; 3.
DR PROSITE; PS50106; PDZ; 3.
SQ SEQUENCE 1205 AA; 132494 MW; 2656704CCEDE8D08 CRC64;

Query Match      6.1%; Score 171.5; DB 4; Length 1205;
Best Local Similarity 20.4%; Pred. No. 0.095;
Matches 94; Conservative 70; Mismatches 146; Indels 151; Gaps 17;

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Db     508 GLGVSELKNGSRGTDLGI:FKSIITHGAAPKGRLEMRNDGLTAVNGESLTGKSNSHEAM 567
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY    88 SLITRAK-----LRSESPMEIAFIQRKSYCGHPGNCICPSPQVSEDGCPQ 132
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     568 ETLRSSMSMEGNIRGMIOVLIRRPMPME----DPACGGAFAKPC-----FENC-Q 614

QY   133 TSTFTLLSSPETLLPKTSTPTQTQDS--TFPSCKAIQTKPEHDKTEHSPTSLDNSPAD 190
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     615 NAVTTTSRRNDNSIIHLPGTCSPQDKQKGLLPNDGMAESEPVPSTPHSAIUGLGLEDYSH 674

QY   191 TSNADIAPMTDDSDSGQGKISLNPP-----SVRLKAELKEMALNYLGIOPTKEQREALR- 244
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     675 SSGVDSAYVFPDQHINFR---SVTPARQPESINLKASK-----SMDLVDPDESKVHSLAG 725

QY   245 EQVGADSKGTYSFGDFVOVAR---SLFLCLQIDENVNVGVEIP-----283
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     726 QXSESFSK---DPGPTGLCLKKSSLESLSQTAAVAEVKRNKLDPHRRPAPHMVGRGCNSFR 782

QY   284 STLDSQLLPDCSLADEV-----GKLRQERNAALJEER 315
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     783 AAIDSXYDGPBEIEADGLSDKSSHSGQALNCESAPOQNSELEDMENKARKVKTKKEKK 842

QY   316 NVLKEKLLESEKHKKQ-----LI 333
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Db     843 KKEGKLVKYEKKKEENEOPERKIKKGFGGAMLRFCKKXEDKCKGAKAQKGLTHHGGLRE 902

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Search completed: October 9, 2003, 11:02:20
Job time : 44.6351 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 10:59:20 ; Search time 282.013 Seconds
(without alignments)
1797.171 Million cell updates/sec

Title: US-09-647-978A-2
Perfect score: 2832
Sequence: 1 MSDGTASRSSPLDRDPAF.....LSCAESEDPCRELTDPKS 557

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
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30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 2832 | 100.0 | 557 | 20 | US-09-647-978A-2 |

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|----|-------|-------|------|----|----------------------|-------------------|
| 2 | 2832 | 100.0 | 557 | 22 | US-09-791-537-144266 | Sequence 144266, |
| 3 | 2109 | 74.5 | 553 | 20 | US-09-647-978A-5 | Sequence 5, Appli |
| 4 | 1345 | 47.5 | 405 | 1 | PCT-US02-22833-13 | Sequence 13, Appl |
| 5 | 1345 | 47.5 | 405 | 1 | PCT-US02-22833A-13 | Sequence 13, Appl |
| 6 | 1193 | 42.1 | 300 | 1 | PCT-US02-28214-1551 | Sequence 1551, Ap |
| 7 | 1193 | 42.1 | 300 | 26 | US-10-012-697-1551 | Sequence 1551, Ap |
| 8 | 639.5 | 22.6 | 256 | 32 | US-60-236-804-455 | Sequence 455, App |
| 9 | 574.5 | 20.3 | 217 | 1 | PCT-US01-47004-181 | Sequence 181, App |
| 10 | 574.5 | 20.3 | 217 | 30 | US-10-416-991-181 | Sequence 181, App |
| 11 | 412 | 14.5 | 150 | 1 | PCT-US01-01329-1354 | Sequence 1354, Ap |
| 12 | 412 | 14.5 | 150 | 1 | PCT-US01-01329-3931 | Sequence 3931, Ap |
| 13 | 412 | 14.5 | 150 | 22 | US-09-764-891-1354 | Sequence 1354, Ap |
| 14 | 412 | 14.5 | 150 | 26 | US-10-080-090-1354 | Sequence 1354, Ap |
| 15 | 412 | 14.5 | 150 | 28 | US-10-205-303-1354 | Sequence 1354, Ap |
| 16 | 195.5 | 6.3 | 1492 | 22 | US-09-791-537-23557 | Sequence 23557, A |
| 17 | 188.5 | 6.7 | 549 | 1 | PCT-US01-08631-33775 | Sequence 33775, A |
| 18 | 187.5 | 6.6 | 1427 | 22 | US-09-791-537-23553 | Sequence 23553, A |
| 19 | 187.5 | 6.6 | 1500 | 22 | US-09-791-537-23560 | Sequence 23560, A |
| 20 | 187.5 | 6.6 | 1743 | 1 | PCT-US01-08631-41287 | Sequence 41287, A |
| 21 | 187.5 | 6.6 | 1743 | 1 | PCT-US01-08656-9308 | Sequence 9308, Ap |
| 22 | 187.5 | 6.6 | 1743 | 28 | US-10-273-573-9308 | Sequence 9308, Ap |
| 23 | 187.5 | 6.6 | 1816 | 28 | US-10-219-051B-2337 | Sequence 2337, Ap |
| 24 | 187.5 | 6.6 | 1816 | 28 | US-10-219-051B-2341 | Sequence 2341, Ap |
| 25 | 187.5 | 6.6 | 1816 | 28 | US-10-219-051B-4973 | Sequence 4973, Ap |
| 26 | 187.5 | 6.6 | 1816 | 28 | US-10-219-051B-13391 | Sequence 13391, A |
| 27 | 187.5 | 6.6 | 1816 | 28 | US-10-219-051B-14543 | Sequence 14543, A |
| 28 | 187.5 | 6.6 | 1816 | 30 | US-10-408-765A-1352 | Sequence 1352, Ap |
| 29 | 187.5 | 6.6 | 1816 | 32 | US-60-389-987-1352 | Sequence 1352, Ap |
| 30 | 187.5 | 6.6 | 1816 | 32 | US-60-412-418-1352 | Sequence 1352, Ap |
| 31 | 184.5 | 6.5 | 549 | 1 | PCT-US01-08631-42643 | Sequence 42643, A |
| 32 | 183.5 | 6.5 | 1333 | 22 | US-09-791-537-23563 | Sequence 23563, A |
| 33 | 182.5 | 6.4 | 762 | 30 | US-10-437-963-122020 | Sequence 122020, |
| 34 | 182.5 | 6.4 | 883 | 26 | US-10-094-749-2707 | Sequence 2707, Ap |
| 35 | 181.5 | 6.4 | 1410 | 22 | US-09-791-537-53271 | Sequence 53271, A |
| 36 | 181.5 | 6.4 | 1410 | 30 | US-10-408-765A-1199 | Sequence 1199, Ap |
| 37 | 181.5 | 6.4 | 1410 | 32 | US-60-389-987-1199 | Sequence 1199, Ap |
| 38 | 181.5 | 6.4 | 1410 | 32 | US-60-412-418-1199 | Sequence 1199, Ap |
| 39 | 181 | 6.4 | 1778 | 1 | PCT-US02-13142-8240 | Sequence 8240, Ap |
| 40 | 181 | 6.4 | 1778 | 27 | US-10-128-714-8240 | Sequence 8240, Ap |
| 41 | 178 | 6.3 | 1296 | 22 | US-09-791-537-23564 | Sequence 23564, A |
| 42 | 178 | 6.3 | 1612 | 9 | US-08-545-860C-48 | Sequence 48, Appl |
| 43 | 178 | 6.3 | 1612 | 9 | US-08-545-860C-48 | Sequence 48, Appl |
| 44 | 178 | 6.3 | 1612 | 10 | US-08-686-059-2 | Sequence 2, Appli |
| 45 | 177.5 | 6.3 | 935 | 22 | US-09-757-781-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-09-647-978A-2
; Sequence 2, Application US/09647978A
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein
; FILE REFERENCE: 09/647,978
; CURRENT APPLICATION NUMBER: US/09/647,978A
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/US99/08568
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/082,454
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Mouse
US-09-647-978A-2

Query Match 100.0%; Score 2832; DB 20; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.1e-207;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MSDGTASARSSPLDRDPAPFRVITVTKETGLGLKILGGINRNEGPLVYIHEVIPGGDCYK 60
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 QY 241 EALREQVQADSKGTSGDFVQVARSFLCQLQDEVNNGVHVEIPSLDQSLPPCDSLEADE 300
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 QY 481 TLLLESKELVRSVRAILDMDCLPYGWEAYTADGKYFINHVTQTTSMIHPVMSALNLS 540
 DB 481 TLLLESKELVRSVRAILDMDCLPYGWEAYTADGKYFINHVTQTTSMIHPVMSALNLS 540
 QY 541 AESEEDCPRELTPDKS 557
 DB 541 AESEEDCPRELTPDKS 557
 RESULT 2
 US-09-791-537-144266
 ; Sequence 144266, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 144266
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-791-537-144266
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 Best Local Similarity 100.0%; Pred. No. 1.1e-207;
 Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MSDGTASARSSPLDRDPAPFRVITVTKETGLGLKILGGINRNEGPLVYIHEVIPGGDCYK 60
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 ; Sequence 5, Application US/09647978A
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert Company
 ; TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein
 ; FILE REFERENCE: 09/647,978
 ; CURRENT APPLICATION NUMBER: US/09/647,978A
 ; CURRENT FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: PCT/US99/08568
 ; PRIOR FILING DATE: 1999-04-19
 ; PRIOR APPLICATION NUMBER: 60/082,454
 ; PRIOR FILING DATE: 1998-04-20
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 553
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-647-978A-5
 Query Match 74.5%; Score 2109; DB 20; Length 553;
 Best Local Similarity 76.5%; Pred. No. 3e-152;
 Matches 427; Conservative 49; Mismatches 76; Indels 6; Gaps 4;
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 DB 1 MNKNTSTVWSPSLLEKDPAFQMITIAKETGLGLKILGGINRNEGPLVYIHEVIPGGDCYK 60
 QY 61 DGRLLKPGDQVLSINKESMIGVSFEAKSIITRAKLRSSESPWEIAFTRQSKYCGHPGNICC 120
 DB 61 DGRLLKPGDQVLSINKESMIGVSFEAKSIITRAKLRSSESPWEIAFTRQSKYCGHPGNICC 120
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 DB 180 PITSLDNSPADTNSADIAPAWTDDSGPGKISLNPSVRLKAEKLEMAINALYLGIOPTKEQ 239

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Qy 540 CABESEEDCPRELTDPKS 557
Db 536 RSENEEDCSRELPNQKS 553

RESULT 4

PCT-US02-22833-13

; Sequence 13, Application PC/TUS0222833

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: LAL, Preeti G.

; APPLICANT: HONNCHHELL, Cynthia D.

; APPLICANT: FORSYTHE, Ian J.

; APPLICANT: WALIA, Narinder K.

; APPLICANT: TANG, Y. Tom

; APPLICANT: BOROMSKY, Mark L.

; APPLICANT: BARROSO, Ines

; APPLICANT: WARREN, Bridget A.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: GIETZEN, Kimberly J.

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: LEE, Ernestine A.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: DUGGAN, Brendan M.

; APPLICANT: TRAN, Bao

; APPLICANT: LI, Joana X.

; APPLICANT: RICHARDSON, Thomas W.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: ZEBARADIAN, Yeganeh

; APPLICANT: TRAN, Uyen K.

; APPLICANT: YAO, Monique G.

; APPLICANT: PETERSON, David P.

; APPLICANT: LUO, Wen

; APPLICANT: LEHR-WASON, Patricia M.

; TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PF-1082 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/22833

; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: US 60/306,020

; PRIOR FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: US 60/308,179

; PRIOR FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: US 60/309,702

; PRIOR FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: US 60/311,476

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: US 60/311,718

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: US 60/311,551

; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/314,798
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/316,639
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/317,996
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2187465CD1
PCT-US02-22833-13

Query Match 47.5%; Score 1345; DB 1; Length 405;
Best Local Similarity 69.5%; Pred. No. 7.3e-94;
Matches 280; Conservative 37; Mismatches 58; Indels 28; Gaps 5;

Qy 1 MSDGTASARSSSPDRDPAPRVITVTKETGLGLKILGGINRNEGPLVYIHEVPGDDCYK 60
Db 1 MNKNTSTVWSPSLLEKDPAPQMITIAKETGLGLKVLGGINRNEGPLVYIHEVPGDDCYK 60
Qy 61 DGRLLKPGDQLVSNKSMIGVSPEEAKSIITRAKLRSSEPMIAPIROKSYCGHPGNICC 120
Db 61 DGRLLKPGDQLVSNKSMIGVSPEEAKSIITRAKLRSSEPMIAPIROKSDMIQIPENLSC 120
Qy 121 PS-POVSEDCGPOTSTFTLLSSPSETLLPKTSTPTQDSTPTPSCAKIOTKPEHDKTEHS 179
Db 121 TSLIEASGEYGPQASTLSLSPSPPEILIPKTSPTKTNNDILSSC---EIKGTYNKTVQI 177
Qy 180 PITSLDMSPADTSDNADIAPAWTDDSGPOGKISLNPVRLKAEKLEMALNYLGIQPTKEQ 239
Db 178 PITS-ENSTVGLSNTDVASAWT-ENYGLQEKISLNPVRFKAEKLEMALNYLGIQPTKEQ 235
Qy 240 REALREOVQADSKGTVSFGDFVQVARSFLCQLDDEVNNGVHIEIPSLDSQLLPCDSLEAD 299
Db 236 HQALRQOVQADSKGTVSFGDFVQVARNLFCQLDDEVNNGVHIEIPSLDSQLLPCDSSEAD 295
Qy 300 EVGKLROERNAALFEERNVLKELLESSEKHKRLIEELQNVKQKAKAVAEETALRSRIHL 359
Db 296 EMERLKCERDDALKEVNTLK-----EAKAVVEETALRSRIHL 333
Qy 360 AEAARQAHGEMDYEIVIRLLEAEVSELKAQLADYSQNKES 402
Db 334 AEAARQAHGEMDYEIVIRLLEAKITELKAQLADYSQNKVS 376

RESULT 5

PCT-US02-22833A-13

; Sequence 13, Application PC/TUS0222833A

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: LAL, Preeti G.

; APPLICANT: HONNCHHELL, Cynthia D.

; APPLICANT: FORSYTHE, Ian J.

; APPLICANT: WALIA, Narinder K.

; APPLICANT: TANG, Y. Tom

; APPLICANT: BOROMSKY, Mark L.

; APPLICANT: BARROSO, Ines

; APPLICANT: YUE, Henry

; APPLICANT: WARREN, Bridget A.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: GIETZEN, Kimberly J.

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: LEE, Ernestine A.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: DUGGAN, Brendan M.

; APPLICANT: TRAN, Bao

```

; APPLICANT: LI, Joana X.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: ZEBARJADIAN, Yeganeh
; APPLICANT: TRAN, Uyen K.
; APPLICANT: YAO, Monique G.
; APPLICANT: PETERSON, David P.
; APPLICANT: LUO, Wen
; APPLICANT: LEHR-MASON, Patricia M.
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1082 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/22833A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/306,020
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/308,179
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/309,702
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/311,476
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,718
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,551
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/314,798
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/316,639
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/317,996
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2187465CD1
PCT-US02-22833A-13

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Query Match 47.5%; Score 1345; DB 1; Length 405;
Best Local Similarity 69.5%; Pred. No. 7.3e-94;
Matches 280; Conservative 37; Mismatches 58; Indels 28; Gaps 5;

QY 1 MSDDTASARSSPLDRDPAFRVITVTKETGLKILGGINNEGRLVYIHEVPGGDCYK 60
DB 1 MNKNTSTVSPSLEKDPAFQMITIAKETGLKVLGGINNEGRLVYIHEVPGGDCYK 60

QY 61 DGLRKPGLVSNKESMIGVSFEAKSIITRAKLRESPEWIEAFIRQKSYCGHPGNC 120
DB 61 DGLRKPGLVSNKESMIGVSFEAKSIITRAKLRESPEWIEAFIRQKSDNIOPENLSC 120

QY 121 PS-PQVSDCGPQTFTLLSPSETLLPKTSSPTQDSTFFPCKAIQTKPEHDKTEHS 179
DB 121 TSLIEASGEYGPQASTLSIFSPPELIPKTSPTKNTNDLLSC---EIKTYNKTQVI 177

QY 180 PITSLONGPADTNSADIAPMTDDSGPQKISLNPSVRLKAELMALNYLGIQPTKEQ 239
DB 178 PITL-ENSTVGLSNTDVSAMT-ENYGLQEKISLNPSVRLKAELMALNYLGIQPTKEQ 235

QY 240 REALREQVQADSKGTYSFGDFVQVARSFLQLDEVNNGVHVEIPSLDSQLLPDCLSEAD 299
DB 236 HQALRQVQADSKGTYSFGDFVQVARNFLQLDEVNNGVHVEIPSLDSQLLPDCLSEAD 295

QY 300 EVGKLRQERNAALEERNVLEKLESEKRRKQLIEQLONVQKAEKAVAEETRALRSRIHL 359
DB 296 EMERLKCERDDALKEVNTLK-----EAKAVVEETRALRSRIHL 333

QY 360 AEAQOAHGMEMDYEEVIRLLEAEVSELKLAQLADYSQNKES 402
DB 334 AEAQOAHGMEMDYEEVIRLLEAEKITELKLAQLADYSQNKES 376

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RESULT 6
PCT-US02-28214-1551
; Sequence 1551, Application PC/TUS0228214
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kabsam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Scott, Beth
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leehkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
; TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
; FILE REFERENCE: 2300-16252
; CURRENT APPLICATION NUMBER: PCT/US02/28214
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/254,648
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/275,668
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 1568
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1551
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-28214-1551

Query Match 42.1%; Score 1193; DB 1; Length 300;
Best Local Similarity 51.8%; Pred. No. 2.1e-82;
Matches 261; Conservative 18; Mismatches 21; Indels 204; Gaps 3;

QY 17 DPAFRVITVTKETGLKILGGINNEGRLVYIHEVPGGDCYKDGRLKPGDOLVSNKE 76
DB 1 DPAFQMITIAKETGLKILGGINNEGRLVYIHEVPGGDCYKDGRLKPGDOLVSNKE 60

QY 77 SMIGVSFEAKSIITRAKLRESPEWIEAFIRQKSYCGHPGNCPSQVSDCGPQTSTF 136
DB 61 SMIGVSFEAKSIITGAKL----- 79

QY 137 TLLSPSETLLPKTSSPTQDSTFFPCKAIQTKPEHDKTEHSPTSLNSPADTNSADI 196
DB 80 ----- 79

QY 197 APMTDDSGPQKISLNPSVRLKAELMALNYLGIQPTKEQREALREQVQADSKGTYS 256
DB 80 -----SQARKEEKEEALNYLGIQPTKEQHQAALRQVQADSKGTYS 121

QY 257 FGDFVQVARSFLQLDEVNNGVHVEIPSLDSQLLPDCLSEADEVQKLRQERNAALEERN 316
DB 122 FGDFVQVARNFLQLDEVNNGVHVEIPSLDSQLLPDCLSEADEVQKLRQERNAALEERN 154

QY 317 VLKELKLESEKRRKQLIEQLONVQKAEKAVAEETRALRSRIHLAEAAQOAHGMEMDYEE 376
DB 155 ---EKLLESQKRLQTEELQNVKQAKAVVEETRALRSRIHLAEAAQOAHGMEMDYEE 211

QY 377 VIRLLEAEVSELKLAQLADYSQNKESVQDLRKRVTVLDCQLRKSEMAKAFKASTERLILG 436
DB 212 VIRLLEAKITELKLAQLADYSQNK----- 235

QY 437 PIEAIQEVLLDSSAPLSTLERRAVLASQTSPLPARNGRSPFATLLLESKELVRSVRAI 496
DB 236 -----SERBAVLASQTSPLPARNGRSPFATLLLESKELVRSVRAI 276

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QY 497 LDMDCLPYCHWEEAYTADGIKYFIN 520
Db 277 LDMDCLPYCHWEEAYTADGIKYFIN 300

RESULT 7
US-10-012-697-1551
; Sequence 1551, Application US/10012697
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Scott, Beth
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Jones, Lee William
; APPLICANT: Stachne-Crain, Birgit
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
; TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
; FILE REFERENCE: 2300-16252
; CURRENT APPLICATION NUMBER: US/10/012.697
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/254,648
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/275,668
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 1568
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1551
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-697-1551

Query Match 42.1%; Score 1193; DB 26; Length 300;
Best Local Similarity 51.8%; Pred. No. 2.1e-82;
Matches 261; Conservative 18; Mismatches 21; Indels 204; Gaps 3;

QY 17 DPAPRVITVTHETGLGKILGINRNEGPLYIHEVTPGGDCYKDGRLKPGDQVLSINKE 76
Db 1 DPAPQMITIAKETGLGLVGLGINRNEGPLYIHEVTPGGDCYKDGRLKPGDQVLSVNSE 60

QY 77 SMIGVSFEAKSIITRAKLRSESPWEIAFIROKSYCGHPGNIICPSPQVSEDCGPOTSTF 136
Db 61 SMIGVSFEAKSIITGAKL----- 79

QY 137 TLLSPSETLPKTSSTPTQODSTFPSCALQATKPEHDKTEHSPITSLONSPADTSNADI 196
Db 80 ----- 79

QY 197 APATWDDSDGPGKISLNPVRLKAEKLEMAINLYGIQPTKEQREALREQVQADSKGTVS 256
Db 80 -----SQARKKEKEEMALNYLGIQPTKEQHQALRQVQADSKGTVS 121

QY 257 PGDFVQVARSFLCLQDENVGVGHEIFSLDSQLLPCDSLEAEVGVKLRQERNALERN 316
Db 122 PGDFVQVARNLFCQLDENVVGAHBSINLDSQ----- 154

QY 317 VLKELLESKHKRLIELQNVKQEKAAVAETRALRSRIHLAAQAORAHGMEMDYEE 376
Db 155 -----EKLSEDKQKQGLTEELQNVKQEKAAVAETRALRSRIHLAAQAORAHGMEMDYEE 211

QY 377 VIRLLEAEVSELKAQADYSDONKESVQDLRKRVTVLDCQLRKSEMARKAFKASTERLLG 436
Db 212 VIRLLEAKITELKAQADYSDQNK----- 235

US-09-647-978a-2.rapm

QY 437 FIEAIQEVLLDSSAPLSTLSERRAVLASQTSPLIARNGRSFPATLLLESKELVRSVRAI 496
Db 236 -----SERRAVLASQTSPLIARNGRSIPATLALLESKELVRSVRAI 276

QY 497 LDMDCLPYCHWEEAYTADGIKYFIN 520
Db 277 LDMDCLPYCHWEEAYTADGIKYFIN 300

RESULT 8
US-60-236-804-455
; Sequence 455, Application US/60236804
; GENERAL INFORMATION:
; APPLICANT: Ladunga, Steven
; APPLICANT: Spier, Eugene
; APPLICANT: Greenberg, Simon
; APPLICANT: Rabkin, Steven
; APPLICANT: Wang, Yu
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000866
; CURRENT APPLICATION NUMBER: US/60/236,804
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1071
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 455
; LENGTH: 256
; TYPE: PRT
; ORGANISM: HUMAN
US-60-236-804-455

Query Match 22.6%; Score 639.5; DB 32; Length 256;
Best Local Similarity 60.2%; Pred. No. 4.6e-40;
Matches 150; Conservative 17; Mismatches 33; Indels 49; Gaps 5;

QY 277 VGVHEIPSTLDSQLPCD---SL--EADVGKLRQERNAALERNVLKELLESKHK 330
Db 25 IDTEIPEI--AKLGCYSYGSTSLIWEADEMELKERCDDALKVENTIKELLESKDKRK 82

QY 331 QLIEELQNVKQEKAAVAETRALRSRIHLAAQAORAHGMEMDYEEVIRLLEAEVSELKA 390
Db 83 QLTEELQNVKQEKAAVAETRALRSRIHLAAQAORAHGMEMDYEEVIRLLEAKITELKA 142

QY 391 QLADYSDONKESVQDLRKRVTVLDCQLRKSEMARKAFKASTERLLGF:EAIQEVLLDSSA 450
Db 143 QLADYSDQNK-----AIQEVSDNST 163

QY 451 PLSTLSERRAVLASQTSPLIARNGRSFPATLLLESKELVRSVRAILDMDCLPYCHWEEAY 510
Db 164 PLSNLSERRAVLASQTSPLIARNGRSIPATLALLESKELVRSVRAILDMDCLPYCHWEEAY 510

QY 511 --TADGIKY 517
Db 224 DGTLDLVRY 232

RESULT 9
PCT-US01-47004-181
; Sequence 181, Application PC/TUS0147004
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-090
; CURRENT APPLICATION NUMBER: PCT/US01/47004
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/728,952
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 181

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3911
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3931

Query Match          14.5%; Score 412; DB 22; Length 150;
Best Local Similarity 61.4%; Pred. No. 5.5e-23;
Matches 94; Conservative 14; Mismatches 39; Indels 6; Gaps 4;

Cy 79 IGVSFEAKSIITRAKLRSPEWELAFIROKSYCGHPGNICCPSPQVSEDCGPQTSTFT 137
Db 1 IGVSFEAKSIITRAKLRSPEWELAFIROKSDNIQPNLSCTSLIEASGEYGPQASTLS 60
Cy 138 LLSPPSETLLPKTSSPTQODSTFPSCAKIOTKPEHDKTEHSPTSLDNSPADTSNADIA 197
Db 61 LFSPPPEILIPKTSSTPKTNDILSSC---EIKTGYNKTVQIPITS-ENSTVGLSNTDVA 116
Cy 198 PAWTDSDSGPGKISLNPSVRLKAEKLEMALNY 230
Db 117 SAWT-ENYGLQEKISLNPSVRFKAEKLEMALNY 148

RESULT 14
US-10-080-090-1354
; Sequence 1354, Application US/10080090
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA120C1
; CURRENT APPLICATION NUMBER: US/10/080,090
; CURRENT FILING DATE: 2002-02-22
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 3506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1354
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-080-090-1354

Query Match          14.5%; Score 412; DB 26; Length 150;
Best Local Similarity 61.4%; Pred. No. 5.5e-23;
Matches 94; Conservative 14; Mismatches 39; Indels 6; Gaps 4;

Cy 79 IGVSFEAKSIITRAKLRSPEWELAFIROKSYCGHPGNICCPSPQVSEDCGPQTSTFT 137
Db 1 IGVSFEAKSIITRAKLRSPEWELAFIROKSDNIQPNLSCTSLIEASGEYGPQASTLS 60
Cy 138 LLSPPSETLLPKTSSPTQODSTFPSCAKIOTKPEHDKTEHSPTSLDNSPADTSNADIA 197
Db 61 LFSPPPEILIPKTSSTPKTNDILSSC---EIKTGYNKTVQIPITS-ENSTVGLSNTDVA 116
Cy 198 PAWTDSDSGPGKISLNPSVRLKAEKLEMALNY 230
Db 117 SAWT-ENYGLQEKISLNPSVRFKAEKLEMALNY 148
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RESULT 15
US-10-205-303-1354
; Sequence 1354, Application US/10205303
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA120C2
; CURRENT APPLICATION NUMBER: US/10/205,303
; CURRENT FILING DATE: 2002-07-26
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 3506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1354
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-205-303-1354

Query Match          14.5%; Score 412; DB 28; Length 150;
Best Local Similarity 61.4%; Pred. No. 5.5e-23;
Matches 94; Conservative 14; Mismatches 39; Indels 6; Gaps 4;

Cy 79 IGVSFEAKSIITRAKLRSPEWELAFIROKSYCGHPGNICCPSPQVSEDCGPQTSTFT 137
Db 1 IGVSFEAKSIITRAKLRSPEWELAFIROKSDNIQPNLSCTSLIEASGEYGPQASTLS 60
Cy 138 LLSPPSETLLPKTSSPTQODSTFPSCAKIOTKPEHDKTEHSPTSLDNSPADTSNADIA 197
Db 61 LFSPPPEILIPKTSSTPKTNDILSSC---EIKTGYNKTVQIPITS-ENSTVGLSNTDVA 116
Cy 198 PAWTDSDSGPGKISLNPSVRLKAEKLEMALNY 230
Db 117 SAWT-ENYGLQEKISLNPSVRFKAEKLEMALNY 148
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Search completed: October 9, 2003, 11:11:44
Job time : 284.013 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:57:36 ; Search time 40.6459 Seconds
(without alignments)
2175.142 Million cell updates/sec

Title: US-09-647-978A-2

Perfect score: 2832

Sequence: 1 MSDGTASAGSSPLDRDPAF.....LSCAESEDPCRELTPDKS 557

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq 19Jun03.*
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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 2832 | 100.0 | 557 | AAV52446 | Murine syntaxin-4 |
| 2 | 2832 | 100.0 | 557 | AAO15046 | Mouse syntaxin 4 i |
| 3 | 2000.5 | 70.6 | 554 | AAO15047 | Human syntaxin 4 i |
| 4 | 574.5 | 20.3 | 217 | ABG66753 | Human novel polype |
| 5 | 412 | 14.5 | 150 | ABG95970 | Human testicular a |
| 6 | 412 | 14.5 | 150 | AAAG5273 | Human reproductive |
| 7 | 243 | 8.6 | 72 | AAO15045 | Human syntaxin 4 i |
| 8 | 188.5 | 6.7 | 549 | ABG03416 | Novel human diagno |
| 9 | 187.5 | 6.6 | 1743 | ABG10928 | Novel human diagno |

| | | | | | | |
|----|-------|-----|------|----|----------|---------------------|
| 10 | 184.5 | 6.5 | 549 | 22 | ABG12284 | Novel human diagno |
| 11 | 183 | 6.5 | 1829 | 20 | AAV07242 | Actin-filament bin |
| 12 | 181 | 6.4 | 1178 | 24 | ABJ26182 | Aspergillus fumiga |
| 13 | 178 | 6.3 | 1612 | 16 | AAE66457 | Chimeric ALL-1/AF- |
| 14 | 178 | 6.3 | 1612 | 18 | AAW24094 | Ras-binding protei |
| 15 | 177.5 | 6.3 | 935 | 23 | AAU99746 | Human ASIP-related |
| 16 | 171 | 6.0 | 2485 | 21 | AAE19143 | Amino acid sequenc |
| 17 | 166.5 | 5.9 | 2466 | 16 | AAE71498 | Human protein tyro |
| 18 | 166.5 | 5.9 | 2466 | 19 | AAW75999 | Intracellular prot |
| 19 | 166.5 | 5.9 | 2466 | 21 | AAV90272 | Human PTPBLI phosph |
| 20 | 165 | 5.8 | 933 | 22 | ABE60762 | Drosophila melanog |
| 21 | 164.5 | 5.8 | 1310 | 21 | AAV59238 | A rod shortened dy |
| 22 | 163.5 | 5.8 | 611 | 22 | ABE61025 | Drosophila melanog |
| 23 | 163 | 5.8 | 441 | 23 | AAU74348 | Human cytoskeleton |
| 24 | 160 | 5.6 | 2168 | 22 | ABE64563 | Drosophila melanog |
| 25 | 159.5 | 5.6 | 891 | 22 | ABE64847 | Drosophila melanog |
| 26 | 159 | 5.6 | 441 | 23 | ABP43546 | Inner centromere p |
| 27 | 158.5 | 5.6 | 1095 | 20 | AAW80359 | An F-actin-combine |
| 28 | 158 | 5.6 | 2056 | 22 | ABE59344 | Drosophila melanog |
| 29 | 157.5 | 5.6 | 1879 | 22 | AAW25750 | Human protein sequ |
| 30 | 156.5 | 5.5 | 1857 | 23 | AAU84350 | Protein MYH11 diff |
| 31 | 156.5 | 5.5 | 2207 | 22 | AAU32041 | Novel human secret |
| 32 | 156 | 5.5 | 862 | 22 | AAU00022 | Human activated T- |
| 33 | 155.5 | 5.5 | 801 | 23 | ABP68963 | Human polypeptide |
| 34 | 155.5 | 5.5 | 1384 | 24 | ABP55413 | Human MDDT-22 prot |
| 35 | 155.5 | 5.5 | 1404 | 24 | ABP55393 | Human MDDT-22 prot |
| 36 | 155 | 5.5 | 460 | 21 | AAE42620 | Human OREX ORF2384 |
| 37 | 155 | 5.5 | 817 | 24 | AAE33672 | Human structural a |
| 38 | 155 | 5.5 | 1235 | 23 | ABE77435 | Human tumour marke |
| 39 | 155 | 5.5 | 1690 | 22 | ABE61144 | Drosophila melanog |
| 40 | 155 | 5.5 | 1690 | 22 | ABE61173 | Drosophila melanog |
| 41 | 154 | 5.4 | 1038 | 23 | AAW48337 | Human kinesin supe |
| 42 | 154 | 5.4 | 1266 | 23 | ABE47965 | PAR-3 (I700F, I701 |
| 43 | 153.5 | 5.4 | 1038 | 23 | ABE73939 | Candida albicans e |
| 44 | 153.5 | 5.4 | 1098 | 22 | ABE11704 | Human semaphorin d |
| 45 | 153.5 | 5.4 | 2633 | 22 | ABG06505 | Novel human diagno |

ALIGNMENTS

RESULT 1
AAV52446
ID AAV52446 standard; protein; 557 AA.
XX
AC AAV52446;
XX
DT 22-FEB-2000 (first entry)
XX
DE Murine syntaxin-4 interacting protein (SYNIP).
XX
KW Syntaxin-4 interacting protein; SYNIP; glucose; transport; GLUT4;
KW vesicle translocation; insulin; regulation; SNARE; SNARE-like;
KW soluble N-ethylmaleimide-sensitive factor attachment protein receptor;
KW uptake; Syntaxin-4; VAMP2; competition; binding; glucose storage;
KW glucose utilisation; recombinant expression; gene therapy; diagnostic;
KW antagonist; agonist; diabetes; glycogen storage disease; obesity;
KW type II; polycystic ovarian syndrome; hypertension; atherosclerosis;
KW insulin resistance; antidiabetic; anorectic; hypotensive;
KW antiarteriosclerotic.
XX
OS Mus sp.
XX
PH Key Location/Qualifiers
FT Domain 19..93 "PDZ domain"
FT Domain /note= "PDZ domain"
FT Domain 219..264
FT Domain /note= "Calcium-binding EF-hand domain"
FT Domain 300..410
FT Domain /note= "Tandem coiled coil domains"
FT Domain 500..533
FT Domain /note= "WW domain"
XX

PN WO9954465-A2.
 XX 28-OCT-1999.
 PD 19-APR-1999; 99WO-US08568
 PP 20-APR-1998; 98US-0082454
 PR (WARN) WARNER LAMBERT CO.
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Min J, Pessin JE, Saltiel AR, Syu L;
 XX WPI; 2000-038498/03.
 DR
 XX Novel polypeptides and polynucleotides used for diagnosis of syndromes
 PT involving abnormal levels of glucose or abnormal GLUT4 translocation .
 PP
 XX Claim 6; Fig 1A; 51pp; English.
 XX
 CC This sequence represents murine syntaxin-4 interacting protein (SYNIP),
 CC which is a novel insulin-regulated SNARE-like protein directly involved
 CC in the regulation of glucose transport and GLUT4 glucose transporter
 CC vesicle translocation. Insulin induces translocation of GLUT4 from the
 CC intracellular low density microsomal compartment to the cell surface,
 CC GLUT4 translocation playing an important role in the uptake of glucose
 CC by cells. Insulin-stimulated glucose transport and GLUT4 translocation
 CC require specific interactions between the vesicle membrane SNARE
 CC (soluble N-ethylmaleimide-sensitive factor attachment protein receptor),
 CC VAMP2, and the target membrane SNARE, syntaxin-4. SYNIPs competitively
 CC bind to syntaxin-4, preventing the ligand from interacting with its
 CC cognate intracellular receptor, and are only expressed in cells which
 CC exhibit insulin-responsive glucose transport and GLUT4 translocation.
 CC Insulin induces a dissociation of the SYNIP:syntaxin-4 complex via a
 CC decrease in the binding affinity of SYNIP for syntaxin-4. Binding of the
 CC SYNIP C-terminal domain is in contrast refractive to insulin stimulation,
 CC but inhibits glucose transport and GLUT4 translocation. SYNIP proteins
 CC and nucleotides may be used in treatment of a variety of disease states
 CC characterised by abnormal GLUT4 translocation or abnormal glucose storage
 CC and/or utilisation. SYNIP nucleotides may be used to recombinantly
 CC express SYNIP proteins, in gene therapy, or as a source of diagnostic
 CC probes and primers. SYNIP proteins may be used to identify antagonists
 CC which will prevent the binding of SYNIP to syntaxin-4, thereby increasing
 CC glucose transport, or agonists, which will act to decrease glucose
 CC transport. The diseases that may be treated include diabetes
 CC (particularly type II), glycogen storage diseases, obesity, polycystic
 CC ovarian syndrome, hypertension, atherosclerosis and other diseases
 CC associated with insulin resistance.
 CC Note: SYNIP cDNAs (mouse and human), and an additional SYNIP protein are
 CC also claimed, but the sequences are not given in the specification.
 XX
 SQ Sequence 557 AA;
 Query Match 100.0%; Score 2832; DB 21; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1.9e-215;
 Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSDGTASAFSSPLDRDPAFRVITVTKETGLKILGKINNEGPLVYIHEVPGDCYK 60
 Db 1 MSDGTASAFSSPLDRDPAFRVITVTKETGLKILGKINNEGPLVYIHEVPGDCYK 60
 QY 61 DGRKPGDOLVINKESMIGVSFEAKSIITRAKLRESPEWEIFAKQSYCGHPGNC 120
 Db 61 DGRKPGDOLVINKESMIGVSFEAKSIITRAKLRESPEWEIFAKQSYCGHPGNC 120
 QY 121 PPSQVEDCGPOTSTFTLLSSPSETLLPKTSSTPOTQDSTFPSCALQTPKHDKTEHSP 180
 Db 121 PPSQVEDCGPOTSTFTLLSSPSETLLPKTSSTPOTQDSTFPSCALQTPKHDKTEHSP 180
 QY 181 ITSLDNSPDTNADITAPAWTDDSGPGKISLNPSVRLKAEKLEMANALYLGIOPTKEQR 240
 Db 181 ITSLDNSPDTNADITAPAWTDDSGPGKISLNPSVRLKAEKLEMANALYLGIOPTKEQR 240

QY 241 EALREQVQADSKGTVSFGDFVQVARSFLCQLQCLDEVAVGVHEIPSIILDSQLPCDSLEADE 300
 Db 241 EALREQVQADSKGTVSFGDFVQVARSFLCQLQCLDEVAVGVHEIPSIILDSQLPCDSLEADE 300
 QY 301 VGKLRORERNAALREBNVLKELLESSEKHKQIIEELQNVKQEKAKAVAEETRALRSRIHLA 360
 Db 301 VGKLRORERNAALREBNVLKELLESSEKHKQIIEELQNVKQEKAKAVAEETRALRSRIHLA 360
 QY 361 EAAQROAHGEMNDYBEVIRLLEAEVSELKAQIADYSDONKESVQDLKRRVTVLDQCLRKS 420
 Db 361 EAAQROAHGEMNDYBEVIRLLEAEVSELKAQIADYSDONKESVQDLKRRVTVLDQCLRKS 420
 QY 421 EMARKAFKASTERLLGFTIATQEVLLDSSAPLSTLSERRAVLASQTSLLPLARNGRSPFA 480
 Db 421 EMARKAFKASTERLLGFTIATQEVLLDSSAPLSTLSERRAVLASQTSLLPLARNGRSPFA 480
 QY 481 TLLLESKELVRSVRAILDMDCLPYGWEAEYTAADGKIYFPIHVTQTTTSWIHPVMSALNLS 540
 Db 481 TLLLESKELVRSVRAILDMDCLPYGWEAEYTAADGKIYFPIHVTQTTTSWIHPVMSALNLS 540
 QY 541 ABESEEDCPRELTDPKS 557
 Db 541 ABESEEDCPRELTDPKS 557
 RESULT 2
 ID AAO15046 standard; Protein; 557 AA.
 AC AAO15046;
 DT 16-AUG-2002 (first entry)
 DE Mouse syntaxin 4 interacting protein.
 KW Mouse; antisense gene therapy; Syntaxin 4 interacting protein;
 KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
 KW inflammation; tumour formation.
 OS Mus musculus.
 PN WO200224864-A2.
 PD 28-MAR-2002.
 PF 19-SEP-2001; 2001WO-US29251.
 FR 22-SEP-2000; 2000US-0668313.
 PA (ISIS-) ISIS PHARM INC.
 PI Monia BP, Freier SM, Wyatt JR;
 DR WPI; 2002-401986/43.
 DR N-PSDB; ABQ62254.
 PT Novel antisense compound that hybridizes and inhibits nucleic acid
 PT molecule encoding Syntaxin 4 interacting protein, useful for treating
 XX diabetes, obesity and skeletal muscle disorder .
 PS Disclosure; Page 95-98; 154pp; English.
 XX The invention comprises antisense oligonucleotides designed to inhibit
 CC expression of Syntaxin 4 interacting protein. The antisense
 CC oligonucleotides of the invention are useful for inhibiting the
 CC expression of Syntaxin 4 interacting protein in cells or tissues. The
 CC antisense oligonucleotides are also useful for treating an animal having
 CC a disease or condition associated with Syntaxin 4 interacting protein
 CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
 CC oligonucleotides can also be used to prevent or delay infection,
 CC inflammation and tumour formation. The present amino acid sequence
 CC represents a mouse Syntaxin 4 interacting protein.

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:57:41 ; Search time 37.3649 Seconds
(without alignments)
3819.179 Million cell updates/sec

Title: US-09-647-978A-5

Perfect score: 2784

Sequence: 1 MNKNTSTVSPVSLLEKDPAF.....LSRSENEEDCSRELPNQKS 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP_TREMBL_23.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phase.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_virus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 2109 | 75.8 | 557 | 11 Q9W89 | Q9W89 mus musculus |
| 2 | 1840 | 66.4 | 533 | 11 Q8CFL1 | Q8CFL1 mus musculus |
| 3 | 1184 | 42.5 | 245 | 4 Q8LV25 | Q8LV25 homo sapien |
| 4 | 187.5 | 6.7 | 3685 | 4 Q14205 | Q14205 homo sapien |
| 5 | 185 | 6.6 | 2003 | 5 Q19658 | Q19658 caenorhabdi |
| 6 | 184 | 6.6 | 1330 | 6 Q97961 | Q97961 vulpes vulp |
| 7 | 183 | 6.6 | 561 | 5 Q95Q64 | Q95Q64 caenorhabdi |
| 8 | 183 | 6.6 | 658 | 5 Q95Q66 | Q95Q66 caenorhabdi |
| 9 | 183 | 6.6 | 721 | 5 P91146 | P91146 caenorhabdi |
| 10 | 182.5 | 6.6 | 802 | 5 Q96398 | Q96398 schistosoma |
| 11 | 182.5 | 6.6 | 1133 | 5 Q21022 | Q21022 caenorhabdi |
| 12 | 181 | 6.5 | 2003 | 5 Q22869 | Q22869 caenorhabdi |
| 13 | 180 | 6.5 | 1319 | 4 Q8TEW2 | Q8TEW2 homo sapien |
| 14 | 180 | 6.5 | 1356 | 4 Q8IN78 | Q8IN78 homo sapien |
| 15 | 179.5 | 6.4 | 1652 | 5 Q8INY8 | Q8INY8 drosophila |
| 16 | 179.5 | 6.4 | 1689 | 5 Q8MSD0 | Q8MSD0 drosophila |

| | | | | | | |
|----|-------|-----|------|----|--------|--------------------|
| 17 | 179.5 | 6.4 | 1690 | 5 | O44929 | O44929 drosophila |
| 18 | 179.5 | 6.4 | 1690 | 5 | Q9VJE5 | Q9VJE5 drosophila |
| 19 | 179.5 | 6.4 | 1308 | 5 | Q9BK91 | Q9BK91 strongyloce |
| 20 | 178 | 6.4 | 1327 | 11 | O61595 | O61595 mus musculu |
| 21 | 175.5 | 6.3 | 819 | 4 | Q8IX28 | Q8IX28 homo sapien |
| 22 | 175.5 | 6.3 | 1031 | 4 | Q9BY57 | Q9BY57 homo sapien |
| 23 | 175.5 | 6.3 | 1353 | 4 | Q9BY58 | Q9BY58 homo sapien |
| 24 | 175.5 | 6.3 | 1940 | 5 | Q02456 | Q02456 schistosoma |
| 25 | 172.5 | 6.2 | 1291 | 17 | Q8TYI2 | Q8TYI2 pyrococcus |
| 26 | 171.5 | 6.2 | 1136 | 4 | Q8TEW8 | Q8TEW8 homo sapien |
| 27 | 171.5 | 6.2 | 2473 | 11 | Q9Q284 | Q9Q284 mus musculu |
| 28 | 171 | 6.1 | 817 | 4 | Q96SB3 | Q96SB3 homo sapien |
| 29 | 169.5 | 6.1 | 1337 | 11 | Q92340 | Q92340 rattus norv |
| 30 | 169 | 6.1 | 1205 | 4 | Q96NX7 | Q96NX7 homo sapien |
| 31 | 169 | 6.1 | 1205 | 4 | Q8IUC7 | Q8IUC7 homo sapien |
| 32 | 169 | 6.1 | 1300 | 4 | Q13999 | Q13999 homo sapien |
| 33 | 169 | 6.1 | 1356 | 4 | Q14707 | Q14707 homo sapien |
| 34 | 169 | 6.1 | 1858 | 5 | Q8MSU5 | Q8MSU5 drosophila |
| 35 | 168.5 | 6.1 | 924 | 5 | O15738 | O15738 dictyosteli |
| 36 | 168.5 | 6.1 | 1475 | 5 | O76447 | O76447 caenorhabdi |
| 37 | 168 | 6.0 | 2139 | 5 | O07569 | O07569 entamoeba h |
| 38 | 167.5 | 6.0 | 876 | 11 | Q8CB21 | Q8CB21 mus musculu |
| 39 | 167.5 | 6.0 | 1333 | 11 | Q99NH2 | Q99NH2 mus musculu |
| 40 | 167.5 | 6.0 | 1871 | 5 | Q9NCL3 | Q9NCL3 drosophila |
| 41 | 167 | 6.0 | 943 | 4 | Q8IX27 | Q8IX27 homo sapien |
| 42 | 166.5 | 6.0 | 980 | 4 | Q9P0K7 | Q9P0K7 homo sapien |
| 43 | 166.5 | 6.0 | 989 | 4 | Q9P2L2 | Q9P2L2 homo sapien |
| 44 | 166.5 | 6.0 | 1099 | 5 | Q9U9K8 | Q9U9K8 dictyosteli |
| 45 | 166 | 6.0 | 795 | 4 | Q9H2G7 | Q9H2G7 homo sapien |

ALIGNMENTS

RESULT 1

Q9WV89 PRELIMINARY; PRT; 557 AA.
ID Q9WV89
AC Q9WV89; (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Syntaxin4-interacting protein synp.
GN STXBPA.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99322667; PubMed=10394363;
RA Min J., Okada S., Kanazaki M., Elmendorf J.S., Coker K.J., Ceresa B.P.,
Syl L.J., Noda Y., Saltiel A.R., Pessin J.E.;
RT "Synp: a novel insulin-regulated syntaxin 4-binding protein mediating
GLUT4 translocation in adipocytes.";
RL Mol. Cell. 3:751-760(1999).
CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF152924; AAD43533.1; --
DR MGD; MGI:1342296; Stxbp4.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00397; WW; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00456; WW; 1.
DR PROSITE; PS01159; WW DOMAIN 1; 1.
DR PROSITE; PS01159; WW DOMAIN 2; 1.
DR PROSITE; PS00020; WW DOMAIN 2; 1.
SQ SEQUENCE 557 AA; 61688 MW; 9211A8B02AF8EC86 CRC64;

Query Match 75.8%; Score 2109; DB 11; Length 557;
Best Local Similarity 76.5%; Pred. No. 6.5e-107;
Matches 427; Conservative 49; Mismatches 76; Indels 6; Gaps 4;

| | | | | | |
|---|---|--|---------------|--|--|
| Qy | 12: | TSLSAEASGEYGPQASTLSLSPSPPEILLIKPTSTSTKTNVNLSSC---EIKTGYNKTVQI | 177 | | |
| Db | 121 | PS-FQVSEDCGPGTSTFTLLSSSEFTLLPKTSTSTPQDSTFPSCKAQTQKPEHCKTEHS | 179 | | |
| Qy | 178 | PITS-ENSTVGLSNTDVASAWT--ENYGLQEKISLNPSPVRFAEKLEEMALNVLGIQPTKEQ | 235 | | |
| Db | 180 | PITSUDNSPADTNSADIAPAWTDGSGPGKISLNPSPVRLKAEKLEEMALNVLGIQPTKEQ | 239 | | |
| Qy | 236 | HQALRQOVQADSKGTVSFGDFVQVARNLFCQLQDEVNNGAHEISNILDSQLLPDSSPAD | 295 | | |
| Db | 240 | REALREQVQADSKGTVSFGDFVQVARSJFCQLQDEVNNGVHEIPSLDSQLLPDCLSEAD | 299 | | |
| Qy | 256 | EMERLKCDERDALKKEVNTLKEKLLBSDKQKQKLTTELQNVKQEAQAVVEETRALRSRTHL | 355 | | |
| Db | 300 | EVGLRQERVAALAEERNVLKKEKLESEKHKQLIEEQNVKQEAQAVABETRALRSRTHL | 359 | | |
| Qy | 356 | AAEAQRAQHGMENDYEEVIRLLLEAKITELKAQADYSDQNKESVQDLKKRIMVLDCQLRK | 415 | | |
| Db | 360 | AAEAQRAQHGMENDYEEVIRLLLEAEVSELKAQADYSDQNKESVQDLKKRITVLDCQLRK | 419 | | |
| Qy | 416 | SEMARKTFEASTKLLHFVETAIQEVESDNSTPLSNLSERRAVLASQTSJLPLGRNGRSIP | 475 | | |
| Db | 420 | SEMARKAFKASTERLLGFIETAIQEVILLDSAPLUSTERRAVLASQTSJLPLLRNGRSFP | 479 | | |
| Qy | 476 | ATLALLESKELVKSVRALLDMDC | 497 | | |
| Db | 480 | ATLLESKELVRSVRALLDMDC | 501 | | |
| RESULT 3 | | | | | |
| Q81VZ5 | | | | | |
| ID | Q81VZ5 | PRELIMINARY; | PRT; 245 AA. | | |
| AC | Q81VZ5 | | | | |
| DT | 01-MAR-2003 | (TrEMBLrel. 23, Created) | | | |
| DT | 01-MAR-2003 | (TrEMBLrel. 23, Last sequence update) | | | |
| DT | 01-MAR-2003 | (TrEMBLrel. 23, Last annotation update) | | | |
| DE | Similar to syntaxin binding protein 4. | | | | |
| OS | Homo sapiens (Human). | | | | |
| CC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| CC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_TaxId=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Eye; | | | | |
| RA | Strausberg R.; | | | | |
| RL | Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; BC041485; AAH41485.1; | | | | |
| SQ | SEQUENCE | 245 AA; 26974 MW; 4E92DDBBFD27DF79 | CRC64; | | |
| Query Match 42.5%; Score 1184; DB 4; Length 245; | | | | | |
| Best Local Similarity 98.8%; Pred. No. 4.4e-57; | | | | | |
| Matches 237; Conservative 0; Mismatches 1; Indels 2; Gaps 1 | | | | | |
| Qy | 78 | MIGVSFEAKSGIITRAKL--RLSEAMEIAFIRKSDNIQENLSCTSTSEASGEYGPQAS | 135 | | |
| Db | 1 | MIGVSFEAKSGIITGAKLSRLSEAMEIAFIRKSDNIQENLSCTSLSEASGEYGPQAS | 60 | | |
| Qy | 136 | TLSLSPSPPEILLIKPTSTSTKTNVNLSSCEIKTGYNKTVQIPITSENSTVGLSNTDVAS | 195 | | |
| Db | 61 | TLSLSPSPPEILLIKPTSTSTKTNVNLSSCEIKTGYNKTVQIPITSENSTVGLSNTDVAS | 120 | | |
| Qy | 196 | ANTENYGLQEKISLNPSPVRFAEKLEEMALNVLGIQPTKEOHQALRQOVQADSKGTVSFGD | 255 | | |
| Db | 121 | ANTENYGLQEKISLNPSPVRFAEKLEEMALNVLGIQPTKEOHQALRQOVQADSKGTVSFGD | 180 | | |
| Qy | 256 | FVQVARNLFCQLQDEVNNGAHEISNILDSQLLPDSSPADMERLKCERDDALKKEVNTLK | 315 | | |
| Db | 181 | FVQVARNLFCQLQDEVNNGAHEISNILDSQLLPDSSPADMERLKCERDDALKKEVNTLK | 240 | | |
| RESULT 4 | | | | | |
| Q14205 | | | | | |
| ID | Q14205 | PRELIMINARY; | PRT; 3685 AA. | | |

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:59:20, Search time 279.987 Seconds
(without alignments)
1797.171 Million cell updates/sec

Title: US-09-647-978A-5

Perfect score: 2784

Sequence: 1 MNKNTSTVSGSLLEKDPAP.....LSRSENEEDCSRELNPQKS 553

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main.*
1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
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22: /cgn2_6/ptodata/1/paa/US097B COMB.pcp.*
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24: /cgn2_6/ptodata/1/paa/US099A COMB.pcp.*
25: /cgn2_6/ptodata/1/paa/US099B COMB.pcp.*
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27: /cgn2_6/ptodata/1/paa/US101 COMB.pcp.*
28: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*
29: /cgn2_6/ptodata/1/paa/US103 COMB.pcp.*
30: /cgn2_6/ptodata/1/paa/US104 COMB.pcp.*
31: /cgn2_6/ptodata/1/paa/US106 COMB.pcp.*
32: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 2784 | 100.0 | 553 | 20 US-09-647-978A-5 | Sequence 5, Appli |

| | | | | | | |
|----|-------|------|------|----|----------------------|-------------------|
| 2 | 2109 | 75.8 | 557 | 20 | US-09-647-978A-2 | Sequence 2, Appli |
| 3 | 2109 | 75.8 | 557 | 22 | US-09-791-537-144266 | Sequence 144266, |
| 4 | 1864 | 67.0 | 405 | 1 | PCT-US02-22833A-13 | Sequence 13, Appl |
| 5 | 1864 | 67.0 | 405 | 1 | PCT-US02-22833A-13 | Sequence 13, Appl |
| 6 | 1312 | 47.1 | 300 | 1 | PCT-US02-28214-1551 | Sequence 1551, Ap |
| 7 | 1312 | 47.1 | 300 | 26 | US-10-012-697-1551 | Sequence 1551, Ap |
| 8 | 866 | 31.1 | 217 | 1 | PCT-US01-47004-181 | Sequence 181, App |
| 9 | 866 | 31.1 | 217 | 30 | US-10-416-991-181 | Sequence 181, App |
| 10 | 780.5 | 28.0 | 256 | 32 | US-09-236-804-455 | Sequence 455, App |
| 11 | 744 | 26.7 | 150 | 1 | PCT-US01-01329-1354 | Sequence 1354, Ap |
| 12 | 744 | 26.7 | 150 | 1 | PCT-US01-01329-1354 | Sequence 1354, Ap |
| 13 | 744 | 26.7 | 150 | 22 | US-09-764-891-3931 | Sequence 3931, Ap |
| 14 | 744 | 26.7 | 150 | 26 | US-10-080-090-1354 | Sequence 1354, Ap |
| 15 | 744 | 26.7 | 150 | 28 | US-10-205-103-1354 | Sequence 1354, Ap |
| 16 | 313 | 11.2 | 549 | 1 | PCT-US01-08631-42643 | Sequence 42643, A |
| 17 | 310 | 11.1 | 549 | 1 | PCT-US01-08631-33775 | Sequence 33775, A |
| 18 | 195 | 7.0 | 561 | 13 | US-08-967-909-2 | Sequence 2, Appli |
| 19 | 190.5 | 6.8 | 1020 | 27 | US-10-179-131-5887 | Sequence 5887, Ap |
| 20 | 190.5 | 6.8 | 1881 | 1 | PCT-US02-03987-15590 | Sequence 15590, A |
| 21 | 190.5 | 6.8 | 1881 | 26 | US-10-032-585-7646 | Sequence 7646, Ap |
| 22 | 190.5 | 6.8 | 1881 | 26 | US-10-072-851-15590 | Sequence 15590, A |
| 23 | 190.5 | 6.8 | 1881 | 32 | US-09-314-050-7646 | Sequence 7646, Ap |
| 24 | 188.5 | 6.8 | 2722 | 21 | US-09-724-676-91394 | Sequence 91394, A |
| 25 | 188.5 | 6.8 | 2722 | 21 | US-09-724-676A-91394 | Sequence 91394, A |
| 26 | 188.5 | 6.8 | 2872 | 21 | US-09-724-676-91401 | Sequence 91401, A |
| 27 | 188.5 | 6.8 | 2872 | 21 | US-09-724-676A-91401 | Sequence 91401, A |
| 28 | 188.5 | 6.8 | 2929 | 21 | US-09-724-676-91386 | Sequence 91386, A |
| 29 | 188.5 | 6.8 | 2929 | 21 | US-09-724-676A-91386 | Sequence 91386, A |
| 30 | 188.5 | 6.8 | 2997 | 21 | US-09-724-676-91405 | Sequence 91405, A |
| 31 | 188.5 | 6.8 | 2997 | 21 | US-09-724-676A-91405 | Sequence 91405, A |
| 32 | 188.5 | 6.8 | 3041 | 21 | US-09-724-676-91393 | Sequence 91393, A |
| 33 | 188.5 | 6.8 | 3041 | 21 | US-09-724-676A-91393 | Sequence 91393, A |
| 34 | 188.5 | 6.8 | 3054 | 21 | US-09-724-676-91391 | Sequence 91391, A |
| 35 | 188.5 | 6.8 | 3054 | 21 | US-09-724-676A-91391 | Sequence 91391, A |
| 36 | 188.5 | 6.8 | 3080 | 21 | US-09-724-676-91380 | Sequence 91380, A |
| 37 | 188.5 | 6.8 | 3080 | 21 | US-09-724-676A-91380 | Sequence 91380, A |
| 38 | 188.5 | 6.8 | 3191 | 21 | US-09-724-676-91400 | Sequence 91400, A |
| 39 | 188.5 | 6.8 | 3191 | 21 | US-09-724-676A-91400 | Sequence 91400, A |
| 40 | 188.5 | 6.8 | 3204 | 21 | US-09-724-676-91399 | Sequence 91399, A |
| 41 | 188.5 | 6.8 | 3204 | 21 | US-09-724-676A-91399 | Sequence 91399, A |
| 42 | 188.5 | 6.8 | 3248 | 21 | US-09-724-676-91385 | Sequence 91385, A |
| 43 | 188.5 | 6.8 | 3248 | 21 | US-09-724-676A-91385 | Sequence 91385, A |
| 44 | 188.5 | 6.8 | 3261 | 21 | US-09-724-676-91384 | Sequence 91384, A |
| 45 | 188.5 | 6.8 | 3261 | 21 | US-09-724-676A-91384 | Sequence 91384, A |

ALIGNMENTS

RESULT 1
US-09-647-978A-5
; Sequence 5, Application US/09647978A
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein.
; FILE REFERENCE: 09/647,978
; CURRENT APPLICATION NUMBER: US/09/647,978A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/US99/08568
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/082,454
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Human
US-09-647-978A-5

Query Match 100.0%; Score 2784; DB 20; Length 553;
Best Local Similarity 100.0%; Pred. No. 4.3e-200;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKNTSTVWSPSLLEKDPAFQMITIAKETGLGLKVLG:NRNEGPLVYIEIIPGGDCYK 60
DB 1 MNKNTSTVWSPSLLEKDPAFQMITIAKETGLGLKVLG:NRNEGPLVYIEIIPGGDCYK 60
QY 61 DGRLLPGDQVLVNVKESMGVSPFEAKSIITRAKLRLSWEIAFIRQSKSYCGHPNICC 120
DB 61 DGRLLPGDQVLVNVKESMGVSPFEAKSIITRAKLRLSWEIAFIRQSKSYCGHPNICC 120
QY 121 TSLIEASGEYGPQASTLSLFSPPPEILIPKTSSTPKTNNDILSSC:---BIKTGYNKTVQI 177
DB 121 TSLIEASGEYGPQASTLSLFSPPPEILIPKTSSTPKTNNDILSSC:---BIKTGYNKTVQI 177
QY 181 SENSTVGLSNTDVASAWNTENYGLQEKISLNPVSFRFAKLEMAALNYLGIQPTKEQHAR 240
DB 181 SENSTVGLSNTDVASAWNTENYGLQEKISLNPVSFRFAKLEMAALNYLGIQPTKEQHAR 240
QY 241 QOVQADSKGTVSFGDFVQVARNLFCQLQDEVNVAHEISNILDQSLPDCSSSEADMERL 300
DB 241 QOVQADSKGTVSFGDFVQVARNLFCQLQDEVNVAHEISNILDQSLPDCSSSEADMERL 300
QY 301 KCRDQALKEVNTLKEKLESQKQKQTEELQNVKQEKAVVEETRALSRHLEAAQ 360
DB 301 KCRDQALKEVNTLKEKLESQKQKQTEELQNVKQEKAVVEETRALSRHLEAAQ 360
QY 361 ROAHGEMDYBEVIRLLEAKITELKAOLADYSDQNKESVQDLKRIWVLDQCLRKSEMAR 420
DB 361 ROAHGEMDYBEVIRLLEAKITELKAOLADYSDQNKESVQDLKRIWVLDQCLRKSEMAR 420
QY 421 KTFEASTKLLHFVEAIOEVFSDNSTPLNSLERRAVLASQTSITPLGRNGRSIPATLAL 480
DB 421 KTFEASTKLLHFVEAIOEVFSDNSTPLNSLERRAVLASQTSITPLGRNGRSIPATLAL 480
QY 481 ESKELVKSVRALLDMDCPLPYGWEAYTAGDKIKYFINHVTTQTSWIHPVMSVLNSRSEEN 540
DB 481 ESKELVKSVRALLDMDCPLPYGWEAYTAGDKIKYFINHVTTQTSWIHPVMSVLNSRSEEN 540
QY 541 EDCSRELPNQKS 553
DB 541 EDCSRELPNQKS 553

RESULT 2

US-09-647-978A-2
; Sequence 2, Application US/09647978A
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein
; FILE REFERENCE: 09/647,978
; CURRENT APPLICATION NUMBER: US/09/647,978A
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/US99/08568
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/082,454
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Mouse
US-09-647-978A-2

Query Match 75.8%; Score 2109; DB 20; Length 557;
Best Local Similarity 76.5%; Pred. No. 2.8e-149;
Matches 427; Conservative 49; Mismatches 76; Indels 6; Gaps 4;

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DB 1 MSDGTASARSSSPLDRDPAPRVITVTKETGLGLKILGGINRNEGPLVYIHEVIPPGGDCYK 60
QY 61 DGRLLPGDQVLVNVKESMGVSPFEAKSIITRAKLRLSWEIAFIRQSKSYCGHPNICC 120

DB 61 DGRLLPGDQVLVNVKESMGVSPFEAKSIITRAKLRLSWEIAFIRQSKSYCGHPNICC 120
QY 121 TSLIEASGEYGPQASTLSLFSPPPEILIPKTSSTPKTNNDILSSC:---BIKTGYNKTVQI 177
DB 121 PS-PQVSEDCGQPTSTFTLLSSPSETLLPKTSSTPQDSTFPSCAKIQTKEHDKTEHS 179
QY 178 PITS-ENSTVGLSNTDVASAWNT-ENYGLQEKISLNPVSFRFAKLEMAALNYLGIQPTKEQ 235
DB 180 PITS-ENSTVGLSNTDVASAWNT-ENYGLQEKISLNPVSFRFAKLEMAALNYLGIQPTKEQ 239
QY 236 HQALRQOVQADSKGTVSFGDFVQVARNLFCQLQDEVNVAHEISNILDQSLPDCSSSEAD 295
DB 240 REALREQVQADSKGTVSFGDFVQVARNLFCQLQDEVNVAHEISNILDQSLPDCSSLEAD 299
QY 296 EMERLKCERDQALKEVNTLKEKLESQKQKQTEELQNVKQEKAVVEETRALSRHLEAAQ 355
DB 300 EVGKLQERNALEERLVLEKLESEKHKQKQTEELQNVKQEKAVVEETRALSRHLEAAQ 359
QY 356 AEAARQAHGEMDYBEVIRLLEAKITELKAOLADYSDQNKESVQDLKRIWVLDQCLRK 415
DB 360 AEAARQAHGEMDYBEVIRLLEAKITELKAOLADYSDQNKESVQDLKRIWVLDQCLRK 419
QY 416 SEMARKTFEASTKLLHFVEAIOEVFSDNSTPLNSLERRAVLASQTSITPLGRNGRSIP 475
DB 420 SEMARKTFEASTKLLHFVEAIOEVFSDNSTPLNSLERRAVLASQTSITPLGRNGRSIP 479
QY 476 ATTALESKELVKSVRALLDMDCPLPYGWEAYTAGDKIKYFINHVTTQTSWIHPVMSVLNS 535
DB 480 ATTALESKELVKSVRALLDMDCPLPYGWEAYTAGDKIKYFINHVTTQTSWIHPVMSVLNS 539
QY 536 RSENEEDCSRELPNQKS 553
DB 540 CAERSEEDCPRELTPDKS 557

RESULT 3

US-09-791-537-144266
; Sequence 144266, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 144266
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-144266

Query Match 75.8%; Score 2109; DB 22; Length 557;
Best Local Similarity 76.5%; Pred. No. 2.8e-149;
Matches 427; Conservative 49; Mismatches 76; Indels 6; Gaps 4;

QY 1 MNKNTSTVWSPSLLEKDPAFQMITIAKETGLGLKVLG:NRNEGPLVYIEIIPGGDCYK 60
DB 1 MSDGTASARSSSPLDRDPAPRVITVTKETGLGLKILGGINRNEGPLVYIHEVIPPGGDCYK 60
QY 61 DGRLLPGDQVLVNVKESMGVSPFEAKSIITRAKLRLSWEIAFIRQSKSYCGHPNICC 120
DB 61 DGRLLPGDQVLVNVKESMGVSPFEAKSIITRAKLRLSWEIAFIRQSKSYCGHPNICC 120
QY 121 TSLIEASGEYGPQASTLSLFSPPPEILIPKTSSTPKTNNDILSSC:---BIKTGYNKTVQI 177
DB 121 PS-PQVSEDCGQPTSTFTLLSSPSETLLPKTSSTPQDSTFPSCAKIQTKEHDKTEHS 179
QY 178 PITS-ENSTVGLSNTDVASAWNT-ENYGLQEKISLNPVSFRFAKLEMAALNYLGIQPTKEQ 235

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:59:50 ; Search time 45.336 Seconds
(without alignments)
1965.413 Million cell updates/sec

Title: US-09-647-978A-5

Perfect score: 2784

Sequence: 1 MNKNTSTVTVSPSLKNDPAF.....LSRSENEEDCSRELPNOKS 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 744 | 26.7 | 150 | 11 | US-09-764-891-3931 |
| 2 | 190.5 | 6.8 | 1881 | 12 | Sequence 3931, Ap |
| 3 | 180 | 6.5 | 1356 | 10 | Sequence 7646, Ap |
| 4 | 175.5 | 6.3 | 935 | 10 | Sequence 2, Appli |
| 5 | 175 | 6.3 | 2485 | 9 | US-09-757-781-1 |
| 6 | 169.5 | 6.1 | 1337 | 10 | US-09-802-669-46 |
| 7 | 169 | 6.1 | 1001 | 15 | US-09-757-781-62 |
| 8 | 167.5 | 6.0 | 1743 | 12 | US-10-128-714-3240 |
| 9 | 167 | 6.0 | 2466 | 12 | US-09-882-227-624 |
| 10 | 161 | 5.8 | 2383 | 15 | US-10-177-980-12 |
| 11 | 158.5 | 5.7 | 1388 | 15 | US-10-082-830-260 |
| 12 | 158 | 5.7 | 2125 | 10 | US-10-446-473-82 |
| 13 | 158 | 5.7 | 2649 | 12 | US-09-919-172-29 |
| 14 | 157 | 5.6 | 1178 | 15 | US-10-205-219-169 |
| 15 | 156.5 | 5.6 | 1948 | 12 | US-10-128-714-8240 |
| | | | | | Sequence 7611, Ap |

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| 16 | 155.5 | 5.6 | 888 | 11 | US-09-893-519A-73 | Sequence 73, Appl |
| 17 | 155 | 5.6 | 967 | 15 | US-10-197-666A-90 | Sequence 90, Appl |
| 18 | 155 | 5.6 | 1591 | 15 | US-10-197-666A-92 | Sequence 92, Appl |
| 19 | 153.5 | 5.5 | 2139 | 9 | US-09-727-384-6 | Sequence 6, Appli |
| 20 | 153.5 | 5.5 | 2139 | 15 | US-10-023-219-4 | Sequence 4, Appli |
| 21 | 152.5 | 5.5 | 2871 | 15 | US-10-146-473-41 | Sequence 41, Appl |
| 22 | 152 | 5.4 | 1786 | 10 | US-09-742-096-3 | Sequence 3, Appli |
| 23 | 150 | 5.4 | 3899 | 15 | US-10-171-311-4 | Sequence 3, Appli |
| 24 | 150 | 5.4 | 3907 | 15 | US-10-171-311-2 | Sequence 2, Appli |
| 25 | 150 | 5.4 | 3925 | 15 | US-10-171-311-8 | Sequence 8, Appli |
| 26 | 150 | 5.4 | 3925 | 15 | US-10-171-311-6 | Sequence 6, Appli |
| 27 | 149.5 | 5.4 | 767 | 10 | US-09-919-497-59 | Sequence 59, Appl |
| 28 | 149.5 | 5.4 | 2037 | 10 | US-09-951-401-3 | Sequence 3, Appli |
| 29 | 149.5 | 5.4 | 2037 | 10 | US-09-922-101-3 | Sequence 3, Appli |
| 30 | 149.5 | 5.4 | 2037 | 10 | US-09-951-402-3 | Sequence 3, Appli |
| 31 | 149 | 5.4 | 709 | 12 | US-10-256-250-15 | Sequence 15, Appl |
| 32 | 149 | 5.4 | 724 | 15 | US-10-211-962-22 | Sequence 22, Appl |
| 33 | 149 | 5.4 | 725 | 11 | US-09-978-309A-47 | Sequence 47, Appl |
| 34 | 149 | 5.4 | 725 | 12 | US-10-256-250-14 | Sequence 14, Appl |
| 35 | 148.5 | 5.3 | 724 | 15 | US-10-211-962-21 | Sequence 21, Appl |
| 36 | 148 | 5.3 | 676 | 12 | US-10-256-250-16 | Sequence 16, Appl |
| 37 | 148 | 5.3 | 1711 | 10 | US-09-771-161A-219 | Sequence 219, App |
| 38 | 148 | 5.3 | 1711 | 10 | US-09-771-161A-220 | Sequence 220, App |
| 39 | 147 | 5.3 | 1940 | 12 | US-03-738-630-99 | Sequence 99, Appl |
| 40 | 146.5 | 5.3 | 1641 | 14 | US-10-017-216-5 | Sequence 5, Appli |
| 41 | 146 | 5.2 | 1938 | 15 | US-10-171-311-164 | Sequence 164, App |
| 42 | 146 | 5.2 | 1945 | 11 | US-09-927-597-2 | Sequence 2, Appli |
| 43 | 146 | 5.2 | 1972 | 15 | US-10-171-311-162 | Sequence 162, App |
| 44 | 146 | 5.2 | 1979 | 11 | US-09-927-597-4 | Sequence 4, Appli |
| 45 | 146 | 5.2 | 2055 | 14 | US-10-017-216-4 | Sequence 4, Appli |

ALIGNMENTS

RESULT 1

US-09-764-891-3931
; Sequence 3931, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3931
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3931

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| Query Match | | 26.7% | Score 744; | DB 11; | Length 150; |
| Best Local Similarity | | 100.0% | Pred. No. 3.3e-47; | | |
| Matches 148; | | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 79 | IGVSFEAKSIITRAKLRLSEAWETAFIRQKSDNIQPNLSCTSLIEASGEYGPQASTLS | 138 | | |
| Db | 1 | IGVSFEAKSIITRAKLRLSEAWETAFIRQKSDNIQPNLSCTSLIEASGEYGPQASTLS | 60 | | |
| Qy | 139 | LFSSPPEILIPKTSPTKNTNDILSSCEIKYKNTVOIPITSENSTVGLNTDVASAWT | 198 | | |
| Db | 61 | LFSSPPEILIPKTSPTKNTNDILSSCEIKYKNTVOIPITSENSTVGLNTDVASAWT | 120 | | |
| Qy | 199 | ENYGLOEKISLNPVSFRFKAELKLEMALNY | 226 | | |
| Db | 121 | ENYGLOEKISLNPVSFRFKAELKLEMALNY | 148 | | |

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:57:41 ; Search time 14.9459 Seconds
(without alignments)
1565.502 Million cell updates/sec

Title: US-09-647-978A-5

Perfect score: 2784

Sequence: 1 MNKNTSTVVSFLLEKPAF.....LSRSENEEDCSRLPNQKS 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents AA:*
- 2: /cgn2_6/prodata/1/aaa/5A.COMB.pep:*
- 3: /cgn2_6/prodata/1/aaa/5B.COMB.pep:*
- 4: /cgn2_6/prodata/1/aaa/5A.COMB.pep:*
- 5: /cgn2_6/prodata/1/aaa/5B.COMB.pep:*
- 6: /cgn2_6/prodata/1/aaa/5A.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 186 | 6.7 | 3248 | 1 | US-08-353-700-1 |
| 2 | 186 | 6.7 | 3248 | 5 | PCT-US95-16216-1 |
| 3 | 185.5 | 6.7 | 2482 | 1 | US-08-328-254-6 |
| 4 | 175 | 6.3 | 2485 | 3 | US-09-290-640-46 |
| 5 | 170.5 | 6.1 | 2465 | 2 | US-08-596-291-3 |
| 6 | 170.5 | 6.1 | 2465 | 3 | US-09-100-804-3 |
| 7 | 168 | 6.0 | 2008 | 4 | US-09-091-501B-8 |
| 8 | 168 | 6.0 | 3433 | 4 | US-09-091-501B-10 |
| 9 | 167 | 6.0 | 976 | 3 | US-09-104-324B-4 |
| 10 | 167 | 6.0 | 2466 | 3 | US-09-080-855-12 |
| 11 | 167 | 6.0 | 2466 | 4 | US-09-566-076-12 |
| 12 | 167 | 6.0 | 2466 | 5 | PCT-US94-09943-2 |
| 13 | 162 | 5.8 | 1829 | 3 | US-09-157-420-1 |
| 14 | 159.5 | 5.7 | 1388 | 4 | US-09-572-193-2 |
| 15 | 159.5 | 5.7 | 1388 | 4 | US-09-723-262-2 |
| 16 | 159.5 | 5.7 | 1388 | 4 | US-09-723-219-2 |
| 17 | 158 | 5.7 | 1612 | 3 | US-08-545-860D-48 |
| 18 | 158 | 5.7 | 1612 | 5 | PCT-US94-04496-48 |
| 19 | 155 | 5.6 | 1184 | 3 | US-09-541-782-2 |
| 20 | 155 | 5.6 | 1184 | 4 | US-09-723-820-2 |
| 21 | 154.5 | 5.5 | 1129 | 4 | US-09-252-991A-29927 |
| 22 | 152 | 5.5 | 896 | 1 | US-08-095-737-2 |
| 23 | 152 | 5.5 | 896 | 1 | US-08-480-145-2 |
| 24 | 152 | 5.5 | 896 | 2 | US-08-477-389-2 |
| 25 | 151 | 5.4 | 1057 | 4 | US-09-107-532A-4789 |
| 26 | 150.5 | 5.4 | 3656 | 4 | US-09-134-001C-5080 |
| 27 | 150 | 5.4 | 1073 | 3 | US-09-541-782-6 |

Sequence 6, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 3, Appli
Sequence 22, Appli
Sequence 21, Appli
Sequence 1, Appli
Sequence 31, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 12, Appli
Sequence 3944, Ap
Sequence 16965, A
Sequence 4, Appli
Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-353-700-1
; Sequence 1, Application US/08353700
; Patent No. 559919
; GENERAL INFORMATION:
; APPLICANT: YEN, TIMOTHY J.
; APPLICANT: RATTNER, JEROME B.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A
; TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
; STREET: 1601 MARKET STREET, SUITE 720
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353.700
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, JANET E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; US-08-353-700-1

Query Match 6.7%; Score 186; DB 1; Length 3248;
Best Local Similarity 21.6%; Pred.No.3.9e-06;
Matches 104; Conservative 80; Mismatches 180; Indels 118; Gaps 19;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:57:36 ; Search time 40.3541 Seconds
(without alignments)
2175.142 Million cell updates/sec

Title: US-09-647-978A-5

Perfect score: 2784

Sequence: 1 MNKNTSTVSPVSLLEKPAF.....LSRSENEEDCSRELPNQKS 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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| 24: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 2549.5 | 91.6 | 554 | 23 | Human syntaxin 4 i |
| 2 | 2109 | 75.8 | 557 | 21 | Murine syntaxin-4 |
| 3 | 2109 | 75.8 | 557 | 23 | Mouse syntaxin 4 i |
| 4 | 866 | 31.1 | 217 | 23 | Human novel polype |
| 5 | 744 | 26.7 | 150 | 22 | Human testicular a |
| 6 | 744 | 26.7 | 150 | 22 | Human reproductive |
| 7 | 313 | 11.2 | 549 | 22 | Novel human diagno |
| 8 | 310 | 11.1 | 549 | 22 | Novel human diagno |
| 9 | 287 | 10.3 | 72 | 23 | Human syntaxin 4 i |

| | | | | | | |
|----|-------|-----|------|----|-----------|---------------------|
| 10 | 195 | 7.0 | 561 | 19 | AAW63043 | Streptococcus uber |
| 11 | 190.5 | 6.8 | 1881 | 23 | ABP73809 | Candida albicans e |
| 12 | 188.5 | 6.8 | 3685 | 10 | AAAP90290 | Human Duchenne mus |
| 13 | 187.5 | 6.7 | 801 | 23 | ABP68963 | Human polyepitide |
| 14 | 187.5 | 6.7 | 1384 | 24 | ABP55413 | Human MDDT-22 prot |
| 15 | 187.5 | 6.7 | 1404 | 24 | ABP55393 | Human MDDT-2 prote |
| 16 | 187.5 | 6.7 | 3685 | 10 | AAAP90373 | Sequence encoded b |
| 17 | 186 | 6.7 | 3248 | 17 | AAAP95795 | Kinetochores protei |
| 18 | 185.5 | 6.7 | 2482 | 16 | AAAP72826 | Human mitotin. Ho |
| 19 | 185.5 | 6.7 | 2482 | 19 | AAAP23996 | Human mitotin amin |
| 20 | 185.5 | 6.7 | 3210 | 24 | ABU07438 | Protein different |
| 21 | 180 | 6.5 | 1341 | 23 | AAU99747 | Human ASIP-related |
| 22 | 179.5 | 6.4 | 1690 | 22 | ABB61144 | Drosophila melanog |
| 23 | 179.5 | 6.4 | 1690 | 22 | ABB61173 | Drosophila melanog |
| 24 | 178 | 6.4 | 1327 | 23 | ABBS7163 | Mouse ischaemic co |
| 25 | 175.5 | 6.3 | 935 | 23 | AAU99746 | Human ASIP-related |
| 26 | 175 | 6.3 | 2485 | 21 | AAAB19343 | Amino acid sequenc |
| 27 | 174 | 6.2 | 1095 | 20 | AAAB80359 | An P-actin-combine |
| 28 | 169.5 | 6.1 | 1310 | 21 | AAAY59238 | A rod shortened dy |
| 29 | 169.5 | 6.1 | 1337 | 23 | AAU99748 | Rat ASIP protein (|
| 30 | 169 | 6.1 | 1001 | 24 | ABJ25582 | Aspergillus fumiga |
| 31 | 168 | 6.0 | 2008 | 18 | AAJ22016 | Utrrophin truncat |
| 32 | 168 | 6.0 | 2013 | 22 | ABBS7964 | Amino acid sequenc |
| 33 | 168 | 6.0 | 3433 | 18 | AAW22017 | Utrrophin. Homo sa |
| 34 | 167.5 | 6.0 | 1743 | 19 | AAW98879 | H. pylori GHPO 175 |
| 35 | 167 | 6.0 | 976 | 22 | AAG66581 | Human SCP-1 mutai |
| 36 | 167 | 6.0 | 976 | 24 | ABP74709 | Human SCP-1 protei |
| 37 | 167 | 6.0 | 2466 | 16 | AAW71498 | Human protein tyro |
| 38 | 167 | 6.0 | 2466 | 19 | AAW75999 | Intracellular prot |
| 39 | 167 | 6.0 | 2466 | 21 | AAU90272 | Human PTP1 phosph |
| 40 | 166.5 | 6.0 | 980 | 24 | ABU03527 | Angiogenesis-assoc |
| 41 | 166 | 6.0 | 795 | 23 | ABP77430 | Human tumour marke |
| 42 | 166 | 6.0 | 1824 | 19 | AAAY20300 | Human microtubule |
| 43 | 165 | 5.9 | 817 | 24 | AAE33672 | Human structural a |
| 44 | 163 | 5.9 | 865 | 22 | ABBS5798 | Human protein sequ |
| 45 | 163 | 5.9 | 865 | 22 | AAG67610 | Amino acid sequenc |

ALIGNMENTS

RESULT 1
AAO15047
ID AAO15047 standard; Protein; 554 AA.
XX AAO15047;
XX
XX 16-AUG-2002 (first entry)
XX
XX Human syntaxin 4 interacting protein 2.
XX
XX Human; antisense gene therapy; Syntaxin 4 interacting protein;
XX antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
XX inflammation; tumour formation.
XX
XX Homo sapiens.
XX
XX WC200224864-A2.
XX
XX 28-MAR-2002.
XX
XX 19-SEP-2001; 2001WO-US29251.
XX
XX 22-SEP-2000; 2000US-0668313.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Wyatt JR;
XX
XX WPI; 2002-401986/43.
XX
XX N-PSDB; ABQ62261.
XX
XX Novel antisense compound that hybridizes and inhibits nucleic acid

PT molecule encoding Syntaxin 4 interacting protein, useful for treating
PT diabetes, obesity and skeletal muscle disorder -
PS Disclosure; Page 100-104; 154pp; English.
XX
CC The invention comprises antisense oligonucleotides designed to inhibit
CC expression of Syntaxin 4 interacting protein. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of Syntaxin 4 interacting protein in cells or tissues. The
CC antisense oligonucleotides are also useful for treating an animal having
CC a disease or condition associated with Syntaxin 4 interacting protein
CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
CC oligonucleotides can also be used to prevent or delay infection,
CC inflammation and tumour formation. The present amino acid sequence
CC represents a human Syntaxin 4 interacting protein.
XX
SQ Sequence 554 AA;
Query Match 91.6%; Score 2549.5; DB 23; Length 554;
Best Local Similarity 93.3%; Pred. No. 1.4e-190;
Matches 519; Conservative 5; Mismatches 27; Indels 5; Gaps 2;
QY 1 MNKNTSTVWSPSLLEKDPAFQMIFIAKETGLGKVLGGINRNEGPIVYQEIIPGDCYK 60
DB 1 MNKNTSTVWSPSLLEKDPAFQMIFIAKETGLGKVLGGINRNEGPIVYQEIIPGDCYK 60
QY 61 DGRLLPGDQLVSNKSMIGVSFEAKSIITRAKLRESAWEIAFIRKSDNIQENLSC 120
DB 61 DGRLLPGDQLVSNKSMIGVSFEAKSIITRAKLRESAWEIAFIRKSR--QHSARKS 118
QY 121 TSLIASEGVEQFQASTLSLSPPEIL---IPKTSSTPKTNNDILSSCEIKTYNKTQVI 177
DB 119 VMYITRSFRIRWTSLSNLIKSFLLLLKYSIPKPSPPKTNNDILSSCEIKTYNKTQVI 178
QY 178 PITSENSTVGLSNTDVASANTENYGLQKISLNPVSFRFAEKLEMANLYGLQPTKEHQ 237
DB 179 PITSENSTVGLSNTDVASANTENYGLQKISLNPVSFRFAEKLEMANLYGLQPTKEHQ 238
QY 238 ALRQVQADSKGTVSFGDFVQVARNLFCQLQDEVNVGAHEISNILDQLPCDSSEADEM 297
DB 239 ALRQVQADSKGTVSFGDFVQVARNLFCQLQDEVNVGAHEISNILDQLPCDSSEADEM 298
QY 298 ERLCERDDALKENYTLKEKLLSDKQKOLTHELQNVKQEAQVETRALRSRIHLAE 357
DB 299 ERLCERDDALKENYTLKEKLLSDKQKOLTHELQNVKQEAQVETRALRSRIHLAE 358
QY 358 AARQAQHGMDYEEVIRLLLEAKITELKAQADYSDQNKESVDLKKRIMVLDCLRKSE 417
DB 359 AARQAQHGMDYEEVIRLLLEAKITELKAQADYSDQNKESVDLKKRIMVLDCLRKSE 418
QY 418 MARXTEASTKLLHFVEATQVFSNDSTPLSNLSERRAVLASQTSITPLGRNGRSIPAT 477
DB 419 MARXTEASTKLLHFVEATQVFSNDSTPLSNLSERRAVLASQTSITPLGRNGRSIPAT 478
QY 478 LALSKEVLKSVRALDMDCLPYGWEAYTAGDKYFIFKHVTOTTSWIHPVMSVLNLSRS 537
DB 479 LALSKEVLKSVRALDMDCLPYGWEAYTAGDKYFIFKHVTOTTSWIHPVMSVLNLSRS 538
QY 538 EENEEDCSRELPNQKS 553
DB 539 EENEEDCSRELPNQKS 554
RESULT 2
AA52446
ID AA52446 standard; protein; 557 AA.
XX
AC AA52446;
XX
DT 22-FEB-2000 (first entry)
XX
XX Murine syntaxin-4 interacting protein (SYNIP).
XX

KW Syntaxin-4 interacting protein; SYNIP; glucose; transport; GLUT4;
KW vesicle translocation; insulin; regulation; SNARE; SNARE-like;
KW soluble N-ethylmaleimide-sensitive factor attachment protein receptor;
KW uptake; syntaxin-4; VAMP2; competition; binding; glucose storage;
KW glucose utilisation; recombinant expression; gene therapy; diagnostic;
KW antagonist; agonist; diabetes; glycogen storage disease; obesity;
KW type II; polycystic ovarian syndrome; hypertension; atherosclerosis;
KW insulin resistance; antidiabetic; anorectic; hypotensive;
KW antiarteriosclerotic.
XX
QS Mus sp.
XX
XX Key Location/Qualifiers
XX Domain 19..93 "PDZ domain"
XX Domain 219..264
XX Domain /note= "Calcium-binding EF-hand domain"
XX Domain 300..410
XX Domain /note= "Tandem coiled coil domains"
XX Domain 500..533
XX Domain /note= "WW domain"
XX
XX WO9954465-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US08568.
XX
XX 20-APR-1998; 98US-0082454.
XX
XX (WARN) WARNER LAMBERT CO.
XX (ICWA) UNIV IOWA RES FOUND.
XX
XX Min J, Pessin JE, Saltiel AR, Syu L;
XX WPI; 2000-038498/03.
XX
XX Novel polypeptides and polynucleotides used for diagnosis of syndromes
XX involving abnormal levels of glucose or abnormal GLUT4 translocation -
XX
XX Claim 6; Fig 1A; 51pp; English.
XX
XX This sequence represents murine syntaxin-4 interacting protein (SYNIP),
XX which is a novel insulin-regulated SNARE-like protein directly involved
XX in the regulation of glucose transport and GLUT4 glucose transporter
XX vesicle translocation. Insulin induces translocation of GLUT4 from the
XX intracellular low density microsomal compartment to the cell surface,
XX GLUT4 translocation playing an important role in the uptake of glucose
XX by cells. Insulin-stimulated glucose transport and GLUT4 translocation
XX require specific interactions between the vesicle membrane SNARE
XX (soluble N-ethylmaleimide-sensitive factor attachment protein receptor),
XX VAMP2, and the target membrane SNARE, syntaxin-4. SYNIPs competitively
XX bind to syntaxin-4, preventing the ligand from interacting with its
XX cognate intracellular receptor, and are only expressed in cells which
XX exhibit insulin-responsive glucose transport and GLUT4 translocation.
XX Insulin induces a dissociation of the SYNIP:syntaxin-4 complex via a
XX decrease in the binding affinity of SYNIP for syntaxin-4. Binding of the
XX SYNIP C-terminal domain is in contrast refractive to insulin stimulation,
XX but inhibits glucose transport and GLUT4 translocation. SYNIP proteins
XX and nucleotides may be used in treatment of a variety of disease states
XX characterised by abnormal GLUT4 translocation or abnormal glucose storage
XX and/or utilisation. SYNIP nucleotides may be used to recombinantly
XX express SYNIP proteins, in gene therapy, or as a source of diagnostic
XX probes and primers. SYNIP proteins may be used to identify antagonists
XX which will prevent the binding of SYNIP to syntaxin-4, thereby increasing
XX glucose transport, or agonists, which will act to decrease glucose
XX transport. The diseases that may be treated include diabetes
XX (particularly type II), glycogen storage diseases, obesity, polycystic
XX ovarian syndrome, hypertension, atherosclerosis and other diseases
XX associated with insulin resistance.
XX Note: SYNIP cDNAs (mouse and human), and an additional SYNIP protein are
XX also claimed, but the sequences are not given in the specification.
XX